

OM protein - protein search, using sw model

Run on: December 13, 2004, 18:48:47 ; Search time 110.978 Seconds  
(without alignments)  
426.682 Million cell updates/sec

Title: US-10-010-942B-2  
Perfect score: 692  
Sequence: 1 MMSPAQFLFLVLWIRETNG.....CWQGTHFPRTFGGGTKLEIK 132

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	692	100.0	132	5	ABG76923	Abg76923 Mouse 3D6
2	655	94.7	238	8	ADM72033	Adm72033 Chimeric
3	653	94.4	238	8	ADP45549	Adp45549 Mouse bin
4	650	93.9	135	5	ABB79729	Abb79729 Anti-Stre
5	644	93.1	239	6	ABP58274	Abp58274 Humanised
6	641	92.6	132	2	AAR12361	Aar12361 Light (ka
7	641	92.6	133	8	ADO00819	Ado00819 Antibody
8	641	92.6	133	8	ADO43845	Ado43845 Light cha
9	640	92.5	132	5	ABG76925	Abg76925 Humanised

10	639	92.3	131	2	AAR12239	Aar12239	Mouse MAb
11	636	91.9	132	6	ABG74244	Abg74244	Mouse ant
12	630	91.0	132	5	ABG76931	Abg76931	Humanised
13	628	90.8	132	2	AAR24712	Aar24712	Sequence
14	606	87.6	142	4	AAE07032	Aae07032	Murine an
15	595	86.0	239	2	AAR24811	Aar24811	Sequence
16	589	85.1	239	7	ADD47025	Add47025	Rat Prote
17	571	82.5	113	4	AAE03751	Aae03751	Murine PS
18	571	82.5	218	4	AAE03756	Aae03756	Chimeric
19	566	81.8	113	8	ADG25828	Adg25828	Anti-CD30
20	566	81.8	114	8	ADG25839	Adg25839	Anti-CD30
21	562	81.2	353	2	AAY06273	Aay06273	Anti Fc a
22	560	80.9	112	4	AAE06946	Aae06946	Murine 1D
23	560	80.9	112	4	AAU09918	Aau09918	Murine mA
24	560	80.9	112	5	ABG75527	Abg75527	Mouse mAb
25	560	80.9	112	5	ADF98231	Adf98231	Murine mA
26	560	80.9	112	7	ABR61865	Abr61865	Mouse MAb
27	560	80.9	112	8	ADQ31246	Adq31246	Murine 1A
28	560	80.9	122	8	ADJ95990	Adj95990	Immunoglo
29	560	80.9	130	8	ADJ95992	Adj95992	Immunoglo
30	560	80.9	238	8	ADM72035	Adm72035	Chimeric
31	560	80.9	257	3	AAB09777	Aab09777	Antiviral
32	559	80.8	112	2	AAY52765	Aay52765	Anti-tiss
33	559	80.8	112	2	AAY52766	Aay52766	Anti-tiss
34	556	80.3	112	4	AAE06991	Aae06991	Human kap
35	555	80.2	112	5	AAO14971	Aao14971	Mouse lig
36	550	79.5	243	2	AAW60769	Aaw60769	Single ch
37	548	79.2	112	2	AAW48248	Aaw48248	A77 anti-
38	548	79.2	112	4	AAB74621	Aab74621	A77 anti-
39	548	79.2	112	4	AAE08554	Aae08554	Murine A7
40	548	79.2	535	2	AAW28491	Aaw28491	Human p53
41	548	79.2	535	2	AAW28492	Aaw28492	Human p53
42	547	79.0	162	7	ADE06760	Ade06760	D13 light
43	546	78.9	112	7	ABR62960	Abr62960	Monoclonal
44	543	78.5	113	6	ABP58270	Abp58270	Humanised
45	543	78.5	219	6	ABP58272	Abp58272	Humanised

# ALIGNMENTS

## RESULT 1

ABG76923

ID ABG76923 standard; protein; 132 AA.

XX

AC ABG76923;

XX

DT 05-NOV-2002 (first entry)

XX

DE Mouse 3D6 VL protein.

XX

KW Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;

KW variable region complementarity determining region; 3D6; 10D5;

KW variable framework region; amyloidogenic disease; Alzheimer's disease;

KW amyloid deposit; variable light chain; VL; variable heavy chain; VH;

KW nootropic; neuroprotective; inhibitor of beta amyloid accumulation;

KW Abeta.

XX  
 OS Mus musculus.  
 XX  
 PN WO200246237-A2.  
 XX  
 PD 13-JUN-2002.  
 XX  
 PF 06-DEC-2001; 2001WO-US046587.  
 XX  
 PR 06-DEC-2000; 2000US-0251892P.  
 XX  
 PA (NEUR-) NEURALAB LTD.  
 PA (AMHP ) WYETH.  
 XX  
 PI Basi G, Saldanha J, Yednock T;  
 XX  
 DR WPI; 2002-519658/55.  
 DR N-PSDB; ABS59426.  
 XX  
 PT Novel light/heavy chain of humanized immunoglobulin for treating  
 PT amyloidogenic disease, has 3D6/10D5 variable region complementarity  
 PT determining regions and variable framework region from human acceptor  
 PT immunoglobulin.  
 XX  
 PS Claim 67; Fig 1; 171pp; English.  
 XX  
 CC The present invention relates to new humanized immunoglobulin (Ig) light  
 CC chain (LC) or heavy chain (HC) comprising variable region complementarity  
 CC determining regions from 3D6/10D5 Ig LC or HC variable region sequence,  
 CC and variable framework region from human acceptor Ig LC or HC sequence.  
 CC The invention is useful for preventing or treating an amyloidogenic  
 CC disease or Alzheimer's disease in a patient. The invention is also useful  
 CC for in vivo imaging amyloid deposits in a patient. The present amino acid  
 CC sequence represents a mouse 3D6/10D5 variable light (VL) chain or  
 CC variable heavy (VH) chain protein of the invention  
 XX  
 SQ Sequence 132 AA;

Query Match 100.0%; Score 692; DB 5; Length 132;  
 Best Local Similarity 100.0%; Pred. No. 6e-55;  
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MMSPAQFLFLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLLDSGKTYLNW	60
Db	1	MMSPAQFLFLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLLDSGKTYLNW	60
Qy	61	LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTFFP	120
Db	61	LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTFFP	120
Qy	121	RTFGGGTKLEIK	132
Db	121	RTFGGGTKLEIK	132

RESULT 2  
 ADM72033

ID ADM72033 standard; protein; 238 AA.  
 XX  
 AC ADM72033;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Chimeric mouse-human antibody M3C11 light chain.  
 XX  
 KW GPC3; glypican 3; anti-GPC3 antibody; cell disruption; anti-cancer;  
 KW cytostatic; M3C11.  
 XX  
 OS Mus sp.  
 OS Homo sapiens.  
 OS Chimeric.  
 XX  
 PN WO2004022739-A1.  
 XX  
 PD 18-MAR-2004.  
 XX  
 PF 04-SEP-2003; 2003WO-JP011318.  
 XX  
 PR 04-SEP-2002; 2002WO-JP008999.  
 XX  
 PA (CHUS ) CHUGAI SEIYAKU KK.  
 XX  
 PI Aburatani H, Midorikawa Y, Nakano K, Ohizumi I, Ito Y, Tokita S;  
 XX  
 DR WPI; 2004-269573/25.  
 DR N-PSDB; ADM72032.  
 XX  
 PT Antibody against the N terminus of glypican 3(GPC3) causes cell  
 PT disruption and is useful as an anticancer agent.  
 XX  
 PS Example 4; SEQ ID NO 18; 122pp; Japanese.  
 XX  
 CC The invention relates to an antibody against the N terminus of glypican 3  
 CC (GPC3). The antibody can be used for causing cell disruption and can be  
 CC used as an anti-cancer agent. The present sequence represents a chimeric  
 CC mouse-human antibody M3C11 light chain.  
 XX  
 SQ Sequence 238 AA;

Query Match 94.7%; Score 655; DB 8; Length 238;  
 Best Local Similarity 94.7%; Pred. No. 2.6e-51;  
 Matches 124; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 MSPAQFLFLLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWL 61  
 |||  
 Db 1 MSPAQFLFLLVLWIRETNGDVVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWL 60  
 Qy 62 LQRPQGSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGFHPR 121  
 |||  
 Db 61 LQRPQGSPKRLIYLVSKLDSGAPDRFTGSGSGTDFTLKISRVEAEDLGIYYCWQGFHPL 120  
 Qy 122 TFGGGTKLEIK 132  
 |||  
 Db 121 TFGAGTKLELK 131



RESULT 3

ADP45549

ID ADP45549 standard; protein; 238 AA.

XX

AC ADP45549;

XX

DT 09-SEP-2004 (first entry)

XX

DE Mouse binding molecule 11C7 light chain SEQ ID NO:3.

XX

KW binding molecule; human; NogoA; NiG; NiG-D20; NogoA\_623-640;

KW nerve repair; neuroprotective; gene therapy;

KW central nervous system injury; CNS injury; neurodegenerative disorder;

KW mouse; antibody.

XX

OS Mus musculus.

XX

PN WO2004052932-A2.

XX

PD 24-JUN-2004.

XX

PF 09-DEC-2003; 2003WO-EP013960.

XX

PR 10-DEC-2002; 2002GB-00028832.

XX

PA (NOVS ) NOVARTIS AG.

PA (NOVS ) NOVARTIS PHARMA GMBH.

PA (UYZU-) UNIV ZUERICH.

XX

PI Barske C, Mir AK, Oertle T, Schnell L, Schwab ME, Vitaliti A;

PI Zurini M;

XX

DR WPI; 2004-468818/44.

XX

PT New binding molecule that binds to the human NogoA polypeptide, NiG, NiG-

PT D20 or NogoA623-640, useful in preparing a composition for treating CNS

PT injury or neurodegenerative disorders.

XX

PS Claim 9; SEQ ID NO 3; 121pp; English.

XX

CC The present invention describes a binding molecule which binds to human  
CC NogoA polypeptide, human NiG, human NiG-D20 or human NogoA\_623-640 with a  
CC dissociation constant of less than 1000nM. Also described: (1) a  
CC polynucleotide encoding the binding molecule; (2) an expression vector or  
CC system comprising the polynucleotide; (3) a host cell comprising the  
CC expression system; (4) a pharmaceutical composition comprising the  
CC binding molecule and a carrier or diluent; and (5) treating diseases  
CC associated with nerve repair. The binding molecule has neuroprotective  
CC activity, and can be used in gene therapy. The binding molecule is useful  
CC in preparing a composition for treating central nervous system (CNS)  
CC injury or neurodegenerative disorders. The present sequence represents a  
CC mouse binding molecule 11C7 light chain, which is used in the  
CC exemplification of the present invention.

XX

SQ Sequence 238 AA;

Query Match 94.4%; Score 653; DB 8; Length 238;  
Best Local Similarity 93.9%; Pred. No. 4e-51;  
Matches 123; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

```
QY      2 MSPAQFLFLLVLWIRETNGYVVMQTPTLTSVTIGQPASISCKSSQSLLDSDGKTYLNWL 61
      |||
Db      1 MSPAQFLFLLVLWIRETSGDVLLTQTPTLTSITIGQPASISCKSSQSLLHSDGKTYLNWL 60

QY      62 LQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGFTHFPR 121
      |||
Db      61 LQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGFTHFPQ 120

QY      122 TFGGGTKLEIK 132
      |||
Db      121 TFGGGTKLEIK 131
```

RESULT 4

ABB79729

ID ABB79729 standard; protein; 135 AA.

XX

AC ABB79729;

XX

DT 29-OCT-2002 (first entry)

XX

DE Anti-Streptococcus mutans surface antigen MAb SWLA3 VL.

XX

KW Streptococcus mutans; monoclonal antibody; MAb; mouse; chimeric antibody;

KW antibody; anticaries; transgenic plant; transgenic animal; caries;

KW immunotherapy; therapy.

XX

OS Mus musculus.

XX

PN US2002068066-A1.

XX

PD 06-JUN-2002.

XX

PF 15-JUN-2001; 2001US-00881823.

XX

PR 20-AUG-1999; 99US-00378577.

XX

PA (SHIW/) SHI W.

PA (MORR/) MORRISON S L.

PA (TRIN/) TRINH K.

PA (WIMS/) WIMS L.

PA (CHEN/) CHEN L.

PA (ANDE/) ANDERSON M H.

XX

PI Shi W, Morrison SL, Trinh K, Wims L, Chen L, Anderson MH;

XX

DR WPI; 2002-565838/60.

DR N-PSDB; ABN84610.

XX

PT Treatment and prevention of dental caries in mammals, in particular

PT humans by orally administering genetically engineered or purified

PT antibodies that bind to surface antigens of carcinogenic organisms.

XX  
 PS Claim 13; Fig 3A; 30pp; English.  
 XX  
 CC The present sequence is the protein sequence of the light chain variable  
 CC region (VL) of the murine monoclonal antibody SWLA3 (IgG), which binds  
 CC specifically to the surface antigens of cariogenic type c Streptococcus  
 CC mutans (ATCC 25175). The monoclonal antibody is produced by SWLA3 (ATCC  
 CC HB 12558) hybridoma cells. In an example from the invention, chimeric  
 CC monoclonal antibody TEFE was produced comprising SWLA3 variable regions  
 CC and human antibody constant regions. Such chimeric monoclonal antibodies  
 CC can be used to prevent or treat dental caries in humans. The antibodies  
 CC engage the effector apparatus of the human immune system when they bind  
 CC cariogenic organisms, resulting in their destruction. The chimeric  
 CC antibodies may be produced in edible plants, in transgenic animals, or in  
 CC chicken eggs for oral ingestion  
 XX  
 SQ Sequence 135 AA;

Query Match 93.9%; Score 650; DB 5; Length 135;  
 Best Local Similarity 93.2%; Pred. No. 4e-51;  
 Matches 123; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMQTPTLTLSTIGQPASISCKSSQSLLDSDGKTYLNW 60  
 |||||  
 Db 1 MMSPAQFLFLLVLWIRETNGDVVMQTPTLTLSTIGQPASISCKSSQSLLDRDGRTYLSW 60  
 Qy 61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGYYCWQGTHFP 120  
 |||||  
 Db 61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGYYCWQGTHFP 120  
 Qy 121 RTFGGGTKLEIK 132  
 ||| |||||:  
 Db 121 LTFGAGTKLELK 132

# RESULT 5

ABP58274

ID ABP58274 standard; protein; 239 AA.

XX

AC ABP58274;

XX

DT 23-OCT-2003 (revised)

DT 31-MAR-2003 (first entry)

XX

DE Humanised 3D6 antibody light chain.

XX

KW Monoclonal antibody; 3D6; complementarity determining region; CDR; mouse;

KW human; humanised antibody; antibody; Alzheimer's disease;

KW Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.

XX

OS Mus sp.

OS Homo sapiens.

OS Chimeric.

XX

FH Key Location/Qualifiers

FT Peptide 1. .20

FT /label= Signal\_peptide

FT Protein 21. .239  
 FT /label= Mature\_peptide  
 FT /note= "the mature light chain is claimed in Claim 5"  
 FT Region 21. .133  
 FT /note= "light chain variable region, claimed in Claim 4"  
 FT Region 44. .59  
 FT /note= "CDR1"  
 FT Region 75. .81  
 FT /note= "CDR2"  
 FT Region 114. .122  
 FT /note= "CDR3"

XX

PN WO200288306-A2.

XX

PD 07-NOV-2002.

XX

PF 26-APR-2002; 2002WO-US011853.

XX

PR 30-APR-2001; 2001US-0287539P.

XX

PA (ELIL ) LILLY & CO ELI.

XX

PI Tsurushita N, Vasquez M;

XX

DR WPI; 2003-183835/18.

DR N-PSDB; ABZ24632, ABZ24634.

XX

PT New humanized forms of mouse 3D6 antibodies, useful for treating Down's  
 PT syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral  
 PT amyloid angiopathy, or for inhibiting formation of or reducing Abeta  
 PT plaque in the brain.

XX

PS Disclosure; Page 12-13; 54pp; English.

XX

CC The present sequence is that of a preferred light chain of a humanised  
 CC antibody of the present invention. In the variable region of this  
 CC sequence, the complementarity determining regions (CDRs) originate from  
 CC murine monoclonal antibody 3D6 and the framework region from human  
 CC germline Vk segment DPK19 and J segment Jk4. Novel humanised antibodies  
 CC of the invention have CDRs from 3D6 and human framework sequences. These  
 CC humanised antibodies have binding affinities (affinity and epitope  
 CC location) approximately the same as those of the mouse 3D6 antibody. The  
 CC invention includes antibodies, single chain antibodies, and their  
 CC fragments, as well as nucleotide sequences, vectors, transformed host  
 CC cells, and methods of using the humanised antibody to treat, prevent,  
 CC alleviate, reverse or otherwise ameliorate symptoms and/or pathology  
 CC associated with Down's syndrome, (pre-)clinical Alzheimer's disease or  
 CC (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or  
 CC reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise  
 CC OS field)

XX

SQ Sequence 239 AA;

Query Match 93.1%; Score 644; DB 6; Length 239;

Best Local Similarity 90.9%; Pred. No. 2.6e-50;

Matches 120; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNW 60  
 |||||:|:| ||:|||||  
 Db 1 MMSPAQFLFLLVLWIRETNGDVVMTQSPLSLPVTLGQPASISCKSSQSLLDSDGKTYLNW 60

Qy 61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTTHFP 120  
 | |||||:|||||:|||||:|||||:|:|  
 Db 61 LQQRPGQSPRRLIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTTHFP 120

Qy 121 RTFGGGTKLEIK 132  
 |||||:|  
 Db 121 RTFGGGTKVEIK 132

RESULT 6

AAR12361

ID AAR12361 standard; protein; 132 AA.

XX

AC AAR12361;

XX

DT 25-MAR-2003 (revised)

DT 15-AUG-1991 (first entry)

XX

DE Light (kappa) chain variable region of murine 4D12 immunoglobulin.

XX

KW Chimeric antibodies; immunoconjugates; HIV; AIDS.

XX

OS Mus musculus.

XX

PN WO9107493-A.

XX

PD 30-MAY-1991.

XX

PF 13-NOV-1989; 89US-00433730.

XX

PR 13-NOV-1989; 89US-00433730.

XX

PA (XOMA ) XOMA CORP.

PA (GREC ) GREEN CROSS CORP.

XX

PI Better MD, Horwitz AH, Ghoshdasti P, Robinson R;

XX

DR WPI; 1991-178105/24.

DR N-PSDB; AAQ12063.

XX

PT New chimeric mouse-human antibodies - used to detect, kill and remove HIV  
 PT -1 antigen from sample.

XX

PS Disclosure; Fig 18; 107pp; English.

XX

CC This is the light (kappa) - chain variable (V) region of a mouse  
 CC monoclonal antibody (MAb), 4D12, and is specific for an HIV-1 viral  
 CC antigen. It is used in the construction of a chimeric MAb comprising  
 CC heavy and light chains having murine V regions and human C regions. The  
 CC chimeric MAbs are more effective than murine MAb 4D12 since they have an  
 CC increased compatibility in humans. The heavy and light chain V-regions  
 CC are joined by manipulating their respective joining (J) regions, to  
 CC generate restriction enzyme recognition sites. The chimeric MAbs can be

CC used as immunoconjugates, in association with e.g. toxins for HIV  
CC treatment. They can also be used in diagnosis of HIV. See also AAQ12056-  
CC 62. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003  
CC to correct PI field.) (Updated on 25-MAR-2003 to correct DR field.)  
XX  
SQ Sequence 132 AA;

Query Match 92.6%; Score 641; DB 2; Length 132;  
Best Local Similarity 90.9%; Pred. No. 2.5e-50;  
Matches 120; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

```
Qy      1 MMSPAQFLFLLVLWIRETNGYVVMQTPTPLTLSTIGQPASISCKSSQSLLDSDGKTYLNW 60  
        |||||  
Db      1 MMSPAQFLFLLVLWIRETNADVMTQTPTPLTLSTIGQPASFSCSKSSQSLLDSDGKTFLNW 60  
  
Qy     61 LLQRPGQSPKRLIYLVS KLDSGV PDRFTGSGSGTDFTLKISR IEAEDLG LYYCWQGTHFP 120  
        |||||:  
Db     61 FLQRPGQSPKRLLYLVS KLDSGV PDRFTGSGSGTDFTLKISRVE AEDLG VYYCWQGS HFP 120  
  
Qy    121 RTFGGGTKLEIK 132  
        ||| ||||::  
Db    121 ITFGAGTKLELR 132
```

Db 1 MMSPAQFLFLLVLWIRETNGDVVMTQTPLTSLVTIGQPASFCKSSQSLLDSGKTFLNW 60

Qy 61 LLQRPQGSPKRLIYLVSKLD SGVPDRFTGSGSGTDFTLKISR IEAEDLGLYYCWQGT HFP 120

|||||:|||||:|||||:|||||:

Qv 121 RTFGGGTKLEIK 132

||| ||||| ::

Db 121 ITFGAGTKLELR 132

## RESULT 7

ADO00819

ID AD000819 standard; protein; 133 AA.

XX

AC ADO00819;

XX

DT 01-JUL-2004 (first entry)

XX

DE     Antibody JRF/cAbeta40/10 light chain variable region, SEQ ID 6.

XX

KW Neuroprotective; Nootropic; Haemostatic; Vaccine; Amyloid-beta 11;

KW beta-amyloid-related disease; Alzheimer's disease; Abeta sectrease;

KW cleavage site; immunogen; murine; antibody; light chain; variable region;

KW JRF/cAbeta40/10.

XX

OS Mus sp.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	Domain	44.	.59
----	--------	-----	-----

```
FT /note= "CDR1"
```

FT	Domain	75.	.81
----	--------	-----	-----

```
FT /note= "CDR2"
```

FT      Domain      114. .122

FT /note= "CDR3"

XX

PN WO2004029629-A1.

XX

PD 08-APR-2004.

XX

PF 27-SEP-2002; 2002WO-EP011062.

XX

PR 27-SEP-2002; 2002WO-EP011062.

XX

PA (JANC ) JANSSEN PHARM NV.  
 XX  
 PI Mercken MH, Vandermeeren MMPP;  
 XX  
 DR WPI; 2004-316180/29.  
 XX  
 PT New N-11 truncated amyloid-beta monoclonal antibodies specific for human  
 PT Amyloid-beta 11 N-terminal site (A-beta11-x peptides), useful for  
 PT diagnosing or treating beta-amyloid-related diseases e.g. Alzheimer's  
 PT disease.  
 XX  
 PS Disclosure; SEQ ID NO 6; 42pp; English.  
 XX  
 CC The present invention relates to an antibody expressed by the hybridoma  
 CC cells J&JPRD/hAbeta11/1 and J&JPRD/hAbeta11/2, which is capable of  
 CC specifically recognizing human Amyloid-beta 11 N-terminal site (i.e.,  
 CC Abeta11-x peptides). The antibody is useful for diagnosing beta-amyloid-  
 CC related diseases. It is particularly useful for prognosing and monitoring  
 CC response to therapy of Alzheimer's disease and other beta-amyloid related  
 CC diseases and in passive immunization as a method for treating such  
 CC diseases. A humanized form of the antibody is useful for manufacturing a  
 CC medicament for treating, preventing or reversing cognitive decline in  
 CC clinical or pre-clinical Alzheimer's Disease, Down's syndrome, Hereditary  
 CC Cerebral Hemorrhage with Amyloidosis of the Dutch-Type, cerebral amyloid  
 CC angiopathy or other beta-amyloid-related diseases, or to inhibit the  
 CC formation of amyloid plaques or the effects of toxic soluble Amyloid-beta  
 CC ; species in humans. It can also be used in assay systems such as  
 CC competitive methods and nephelometry. The present sequence was used to  
 CC illustrate the invention.  
 XX  
 SQ Sequence 133 AA;

Query Match 92.6%; Score 641; DB 8; Length 133;  
 Best Local Similarity 91.7%; Pred. No. 2.6e-50;  
 Matches 121; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLW 60  
 |||||:|||||  
 Db 1 MMSPAQFLFLVLWIRETNGDVVMQTPLTLAVTIGQPASISCKSGQSLLDGKTYLSW 60  
 Qy 61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTTHFP 120  
 |||||:|||||:|||||  
 Db 61 LLQRPQGSPKRLIYLVSKLDSGVPDRFSGSGSGTDFTLKINRVEAEDLGVYYCWQGTTHFP 120  
 Qy 121 RTFGGGTKLEIK 132  
 |||||  
 Db 121 RTFGGGTNLEIK 132

RESULT 8  
 ADO43845  
 ID ADO43845 standard; protein; 133 AA.  
 XX  
 AC ADO43845;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX

DE Light chain variable region of anti-amyloid-beta antibody.  
XX  
KW antibody; Amyloid-beta11-x peptide; BACE-1; amyloid-beta; beta-secretase;  
KW beta-amyloid precursor protein; beta-amyloid-related disease;  
KW Alzheimer's disease; vaccine; Down's syndrome;  
KW hereditary cerebral haemorrhage; amyloidosis;  
KW cerebral amyloid angiopathy; amyloid plaque.  
XX  
OS Mus sp.  
XX  
FH Key Location/Qualifiers  
FT Region 44. .59  
FT /note= "CDR1"  
FT Region 75. .81  
FT /note= "CDR2"  
FT Region 114. .122  
FT /note= "CDR3"  
XX  
PN WO2004029630-A1.  
XX  
PD 08-APR-2004.  
XX  
PF 09-SEP-2003; 2003WO-EP010092.  
XX  
PR 27-SEP-2002; 2002WO-EP011062.  
XX  
PA (JANC ) JANSSEN PHARM NV.  
XX  
PI Mercken MH, Vandermeeren MMPP;  
XX  
DR WPI; 2004-316181/29.  
XX  
PT New N-11 truncated amyloid-beta monoclonal antibodies specific for human  
PT Amyloid-beta 11-x peptides (A-beta11-x peptides), useful for diagnosing  
PT or treating beta-amyloid-related diseases e.g., Alzheimer's disease.  
XX  
PS Disclosure; Page 38-39; 50pp; English.  
XX  
CC The specification describes a monoclonal antibody which specifically  
CC recognizes human Amyloid-beta11-x peptides. These peptides result from  
CC overexpression of BACE-1 which causes additional cleavage at the +11 site  
CC of amyloid-beta, generating shorter fragments known as Amyloid-beta11-x  
CC peptides. BACE-1 is the major beta-secretase required for cleavage of  
CC beta-amyloid precursor protein. The antibody is useful for detecting the  
CC presence of amyloid-beta peptides in a tissue or fluid sample and for  
CC diagnosing beta-amyloid-related diseases. It is particularly useful for  
CC prognosing and monitoring response to therapy of Alzheimer's disease and  
CC other beta-amyloid related diseases and in passive immunization as a  
CC method for treating such diseases. A humanized form of the antibody is  
CC useful for manufacturing a medicament for treating, preventing or  
CC reversing cognitive decline in clinical or pre-clinical Alzheimer's  
CC Disease, Down's syndrome, Hereditary Cerebral Haemorrhage with  
CC Amyloidosis of the Dutch-Type, cerebral amyloid angiopathy or other beta-  
CC amyloid-related diseases, or to inhibit the formation of amyloid plaques  
CC or the effects of toxic soluble Amyloid-beta species in humans. The  
CC present sequence represents the light chain variable region of an  
CC antibody that recognises amyloid-beta-40 and amyloid-beta11-x peptide







PR 13-NOV-1989; 89US-00433703.

XX

PA (XOMA ) XOMA CORP.

PA (GREC ) GREEN CROSS CORP.

PA (ZOMA-) ZOMA CORP.

XX

PI Better MD, Horwitz AH, Ghoshdasti P, Robinson RR;

XX

DR WPI; 1991-178106/24.

DR N-PSDB; AAQ12019.

XX

PT New chimeric mouse human antibodies - used in treatment, diagnosis and  
PT prophylaxis of HIV infections.

XX

PS Disclosure; Fig 18; 108pp; English.

XX

CC The mouse VL gene product may be used to produce chimeric mouse- human  
CC Abs against HIV-1 comprising human Ig constant regions and murine  
CC variable regions. These novel sequence are useful in treatment, diagnosis  
CC and prophylaxis of HIV infections, and may be produced by a bacterial,  
CC yeast or mammalian expression system. (Updated on 25-MAR-2003 to correct  
CC PA field.) (Updated on 25-MAR-2003 to correct PI field.)

XX

SQ Sequence 131 AA;

Query Match 92.3%; Score 639; DB 2; Length 131;

Best Local Similarity 91.6%; Pred. No. 3.8e-50;

Matches 120; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLVLWIRETNGYVVMQTPTLTLSTIGQPASISCKSSQSLDSDGKTYLWN 60  
|||||

Db 1 MMSPAQFLFLVLWIRETNGDVVMQTPTLTLSTIGQPASFCKSSQSLDSDGKTFLWN 60

Qy 61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTTHFP 120  
|||||

Db 61 FLQRPQGSPKRLLYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGSHP 120

Qy 121 RTFGGGTKLEI 131  
|||

Db 121 ITFGAGTKLEL 131

#### RESULT 11

ABG74244

ID ABG74244 standard; protein; 132 AA.

XX

AC ABG74244;

XX

DT 22-APR-2003 (first entry)

XX

DE Mouse antibody 3D8 light chain variable region.

XX

KW T-cell receptor; cytostatic; dermatological; neuroprotective;

KW immunostimulant; GD3; ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4;

KW 3E11; prostate-specific membrane antigen; zeta signalling chain;

KW CD8alpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer;

KW small cell lung cancer; light chain variable region; mouse.

XX  
OS Mus sp.  
XX  
PN US2002132983-A1.  
XX  
PD 19-SEP-2002.  
XX  
PF 10-DEC-2001; 2001US-00006773.  
XX  
PR 30-NOV-2000; 2000US-0250087P.  
PR 30-NOV-2000; 2000US-0250089P.  
XX  
PA (JUNG/) JUNGHANS R P.  
XX  
PI Junghans RP;  
XX  
DR WPI; 2003-208946/20.  
DR N-PSDB; ABX16570.  
XX  
PT New chimeric molecule useful in treating patients with disorders, such as  
PT melanoma, neuroendocrine disorders, prostate and small cell lung cancer  
PT comprises GD3 and/or PSMA binding domains of antibody.  
XX  
PS Disclosure; Page 13; 35pp; English.  
XX  
CC The invention relates to a chimaeric molecule comprising the GD3  
CC (ganglioside antigen) binding domain of antibody MB3.6, with any of 3  
CC variable gene sequences, or the PSMA (prostate-specific membrane antigen)  
CC binding domain of antibody 3D8, 4D4 and 3E11, with variable gene  
CC sequences, the zeta signalling chain of the T cell receptor and an  
CC intervening CD8alpha hinge in which cysteine residues have been mutated.  
CC The chimaeric molecules expressed in T cells or NK cells or other  
CC effector cells are useful in treating patients with cancers expressing  
CC the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),  
CC and/or together with each other or with heterologous constructs to engage  
CC additional stimulatory and functional properties of the effector cells to  
CC enhance the antitumour therapeutic efficacy (claimed). They are  
CC particularly useful in disorders including melanoma, neuroendocrine  
CC tumours and prostate and small cell lung cancer. The present sequence  
CC represents the mouse antibody 3D8 light chain variable region  
XX  
SQ Sequence 132 AA;

Query Match 91.9%; Score 636; DB 6; Length 132;  
Best Local Similarity 93.9%; Pred. No. 7.2e-50;  
Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 MSPAQFLFLLVLWIRETNGYVMTQTPLTSLVTIGQPASISCKSSQSLLDSGKTYLNWL 61  
|||||:|||||  
Db 1 MSPAQFLFLLVLWIQETNGDVMTQTPLTSLVTIGQPASISCKSSQSLLYSNGKTYLNWL 60  
Qy 62 LQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGFTHFPR 121  
|||||:|||||:|||||  
Db 61 LQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCVQGFTHFPH 120  
Qy 122 TFGGGTKLEIK 132  
|||||

Db 121 TFGGGTKLEIK 131

RESULT 12

ABG76931

ID ABG76931 standard; protein; 132 AA.

XX

AC ABG76931;

XX

DT 05-NOV-2002 (first entry)

XX

DE Humanised 3D6 light chain variable region #2.

XX

KW Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;

KW variable region complementarity determining region; 3D6; 10D5;

KW variable framework region; amyloidogenic disease; Alzheimer's disease;

KW amyloid deposit; variable light chain; VL; variable heavy chain; VH;

KW nootropic; neuroprotective; inhibitor of beta amyloid accumulation;

KW Abeta.

XX

OS Homo sapiens.

OS Mus musculus.

OS Synthetic.

XX

PN WO200246237-A2.

XX

PD 13-JUN-2002.

XX

PF 06-DEC-2001; 2001WO-US046587.

XX

PR 06-DEC-2000; 2000US-0251892P.

XX

PA (NEUR-) NEURALAB LTD.

PA (AMHP ) WYETH.

XX

PI Basi G, Saldanha J, Yednock T;

XX

DR WPI; 2002-519658/55.

XX

PT Novel light/heavy chain of humanized immunoglobulin for treating

PT amyloidogenic disease, has 3D6/10D5 variable region complementarity

PT determining regions and variable framework region from human acceptor

PT immunoglobulin.

XX

PS Claim 55; Page 157; 171pp; English.

XX

CC The present invention relates to new humanized immunoglobulin (Ig) light  
CC chain (LC) or heavy chain (HC) comprising variable region complementarity

CC determining regions from 3D6/10D5 Ig LC or HC variable region sequence,

CC and variable framework region from human acceptor Ig LC or HC sequence.

CC The invention is useful for preventing or treating an amyloidogenic

CC disease or Alzheimer's disease in a patient. The invention is also useful

CC for in vivo imaging amyloid deposits in a patient. The present amino acid

CC sequence represents a humanized 3D6 variable light (VL) chain or variable

CC heavy (VH) chain protein of the invention

XX

SQ Sequence 132 AA;

Query Match 91.0%; Score 630; DB 5; Length 132;  
 Best Local Similarity 89.4%; Pred. No. 2.5e-49;  
 Matches 118; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMQTPTLTLSTIGQPASISCKSSQSLLDSDGKTYLNW 60  
 |||||:|:| || |:|||||  
 Db 1 MMSPAQFLFLLVLWIRETNGDVVMTQSPLSLPVTGPGEPAISCKSSQSLLDSDGKTYLNW 60

Qy 61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120  
 |||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 61 LLQKPGQSPQRILIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGYYCWQGTHFP 120

Qy 121 RTFGGGTKLEIK 132  
 |||| |||:|  
 Db 121 RTFGQGTKVEIK 132

# RESULT 13

AAR24712

ID AAR24712 standard; protein; 132 AA.

XX

AC AAR24712;

XX

DT 25-MAR-2003 (revised)

DT 28-DEC-1992 (first entry)

XX

DE Sequence encoded by the genomic FIB1-11 kappa chain variable (VFK) gene.

XX

KW Chimeric monoclonal antibody; anti-fibrin antibody; PCR;

KW antithrombotic agent; myocardial infarction therapy.

XX

OS Mus musculus.

XX

FH Key Location/Qualifiers

FT Peptide

1. .20

FT /label= leader

FT Region 21. .43

FT /label= Framework Region (FR) 1

FT Region 44. .59

FT /label= complementarity determining region(CDR)1

FT Region 60. .74

FT /label= FR-2

FT Region 75. .81

FT /label= CDR-2

FT Region 82. .112

FT /label= FR-3

FT Region 113. .122

FT /label= CDR-3

FT Region 123. .132

FT /label= FR-4

XX

PN EP491351-A2.

XX

PD 24-JUN-1992.

XX

PF 17-DEC-1991; 91EP-00121591.

XX 18-DEC-1990; 90JP-00413829.  
PR 11-NOV-1991; 91JP-00294464.  
XX  
PA (TAKE ) TAKEDA CHEM IND LTD.  
XX  
PI Iwasa S, Tada H, Watanabe T;  
XX  
DR WPI; 1992-209528/26.  
DR N-PSDB; AAQ25665.  
XX  
PT Chimeric monoclonal antibodies - contain anti-human fibrin antibody light  
PT and heavy chain variable and constant for treating thrombotic conditions  
PT e.g. myocardial infarction.  
XX  
PS Example; Fig 1; 87pp; English.  
XX  
CC A genomic DNA library was prepd. from mouse anti-human fibrin specific  
CC antibody producer hybrid FIB1-11. Screening using a 32P- labeled mouse  
CC JK4-5 gene fragment as a hybridisation probe gave three positive  
CC recombinant phage clones. Phage clone KE14 was identified as a clone  
CC contg. a 15kb fragment coding for the VFK gene. The phage clone KE14 was  
CC subcloned in the plasmid vector pUC119 and sequenced. VFK was a  
CC functional VK gene formed by recombination between the VK gene belonging  
CC to the Subgroup II (VKII) and the JK2 gene (see AAQ25665). (Updated on 25  
CC -MAR-2003 to correct PN field.)  
XX  
SQ Sequence 132 AA;

Qy	1	MMSPAQFLFLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNW	60
Db	1	MMSPAQFLFLLVLWIRETNGDVVMAQTPLTLSVTIGQPAFISCTSSQSLLDSDGKTYLNW	60
Qy	61	LLQRPQGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGT HFP	120
Db	61	LLQRPQGQSPKRLIYLVSKLYSGVPDRFTGSGSGTAFTLKINRVEAEDLG VYYCWQGIHFP	120
Qy	121	RTFGGGTKLEIK	132
Db	121	YTFGGGKLEIK	132

KW neuroprotective; immunosuppressive; human immunodeficiency virus;  
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;  
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;  
 KW multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;  
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;  
 KW fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS;  
 KW inflammatory glomerulopathy; vascular intervention;  
 KW neointimal hyperplasia; antibody 1D9 kappa light chain variable region.  
 XX  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1. .17  
 FT /label= Signal\_peptide  
 FT Protein 18. .142  
 FT /note= "Murine mature antibody 1D9 kappa light chain  
 FT variable region"  
 FT Region 18. .130  
 FT /label= Variable\_region  
 FT Region 131. .142  
 FT /label= Constant\_region  
 XX  
 PN WO200157226-A1.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 02-FEB-2001; 2001WO-US003537.  
 XX  
 PR 03-FEB-2000; 2000US-00497625.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;  
 XX  
 DR WPI; 2001-488888/53.  
 DR N-PSDB; AAD13177.  
 XX  
 PT Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated  
 PT disorder in a patient, comprises a binding specificity for CCR2, and a  
 PT non-human antigen binding region and human immunoglobulin.  
 XX  
 PS Disclosure; Fig 22; 183pp; English.  
 XX  
 CC The patent discloses a humanised antibody or its antigen-binding  
 CC fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),  
 CC comprising an antigen binding region of non-human origin and at least a  
 CC portion of an immunoglobulin of human origin. The humanised antibodies  
 CC are useful for inhibiting the interaction of a cell expressing CCR2. They  
 CC are useful for inhibiting or treating HIV infection. The proteins of the  
 CC invention are useful for inhibiting leukocyte trafficking, for treating  
 CC CCR2-mediated disorders such as inflammatory disorder, autoimmune  
 CC disorders such as rheumatoid arthritis and multiple sclerosis,  
 CC atherogenesis and atherosclerosis, and for inhibiting restenosis. They  
 CC are useful in therapy or diagnosis, and in the manufacture of a  
 CC medicament for treating CCR-2 mediated disease. They are also useful for  
 CC treating allergy, anaphylaxis, malignancy, chronic and acute  
 CC inflammation, histamine and IgE- mediated allergic reaction, shock,



CC stenosis, allograft rejection, fibrotic disease, asthma, inflammatory  
 CC glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis  
 CC associated with vascular intervention, including angioplasty and/or stent  
 CC placement in a mammal. Humanised antibodies are also useful for  
 CC inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting  
 CC neointimal hyperplasia of a vessel in a mammal, preferably associated  
 CC with vascular intervention. The present sequence is murine antibody 1D9  
 CC kappa light chain variable region

XX

SQ Sequence 142 AA;

Query Match 87.6%; Score 606; DB 4; Length 142;  
 Best Local Similarity 93.5%; Pred. No. 4.1e-47;  
 Matches 115; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 10 LLVLWIRETNGYVVMQTPTLTSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPQGSP 69  
 ||||| | |||||:| |||||:|||||  
 Db 7 LLVLWIRETIGDVVMQTPTLTSVTVGHPASISCKSSQSLLDSDGKTFLNWLLQRPQGSP 66

Qy 70 KRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHTFPRTFGGGTKL 129  
 |||||:|||||:|||||  
 Db 67 KRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGYYCWQGTHTFPYTFGGGTKL 126

Qy 130 EIK 132  
 |||  
 Db 127 EIK 129

# RESULT 15

AAR24811

ID AAR24811 standard; protein; 239 AA.

XX

AC AAR24811;

XX

DT 25-MAR-2003 (revised)

DT 28-DEC-1992 (first entry)

XX

DE Sequence encoded by the chimeric kappa chain cDNA (lgkv) contained in  
 DE pTB1427.

XX

KW Chimeric monoclonal antibody; anti-fibrin antibody; primer;  
 KW antithrombotic agent; myocardial infarction therapy.

XX

OS Synthetic.

XX

Key	Location/Qualifiers
FT Peptide	1. .20
FT	/label= leader
FT Region	21. .133
FT	/label= V-kappa
FT Misc-difference	130
FT	/note= "Alternatively = Glu"
FT Region	134. .239
FT	/label= C-kappa

XX

PN EP491351-A2.

XX

PD 24-JUN-1992.  
XX  
PF 17-DEC-1991; 91EP-00121591.  
XX  
PR 18-DEC-1990; 90JP-00413829.  
PR 11-NOV-1991; 91JP-00294464.  
XX  
PA (TAKE ) TAKEDA CHEM IND LTD.  
XX  
PI Iwasa S, Tada H, Watanabe T;  
XX  
DR WPI; 1992-209528/26.  
DR N-PSDB; AAQ25691.  
XX  
PT Chimeric monoclonal antibodies - contain anti-human fibrin antibody light  
PT and heavy chain variable and constant for treating thrombotic conditions  
PT e.g. myocardial infarction.  
XX  
PS Example; Fig 9; 87pp; English.  
XX  
CC Poly(A)+ RNA was prep'd. from the anti-fibrin chimeric Ab-producing  
CC transformant FIB1-H01/X63 and used as a template to clone human C-kappa  
CC cDNA, using the oligo-dT (Pharmacia) primer as a primer for first strand  
CC cDNA synthesis and the 3'E-kappa and 5'C-kappa primers for the PCR. An  
CC amplified DNA fragment of about 0.33kb was isolated and used to create a  
CC C-kappa cDNA contg. vector, pTB1394. Using the same technique, with the  
CC 3'E-kappa primer as a primer for first strand synthesis and the 5'L-kappa  
CC and 3'C-kappa primers for the PCR, an anti-fibrin V-kappa (V-kappa-v)  
CC cDNA was amplified. Furthermore, using the 3'E-kappa primer for first  
CC stand synthesis and the 5'mV-kappa and 3'mV-kappa primers for the PCR, an  
CC anti-fibrin V-kappa cDNA (V-kappa-FIB) was amplified. In addition, a  
CC leader sequence cDNA (L-kappa) was amplified using the 3'C-kappa as a  
CC primer for first strand synthesis and the 5'S-kappa and 3'L- kappa  
CC primers for the PCR. The amplified gene fragments (L-kappa: V-kappa-v: V-  
CC kappa-FIB) were isolated and used to construct respectively plasmids  
CC pTB1391, pTB1392, and pTB1393. L-kappa, V- kappa and C-kappa were joined  
CC together to give a plasmid, pTB1427, contg. the whole length of the  
CC chimeric kappa chain cDNA. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 239 AA;

Qy	1	MMSPAQFLFLVLWIRE	1	MMSPAQFLFLVLWIRE	60
Db	1	MMSPAQFLFLVLWIRE	1	MMSPAQFLFLVLWIRE	60
Qy	61	LLQRPQGSPKRLIYLV	61	LLQRPQGSPKRLIYLV	120
Db	61	LLQRPQGSPRRLIYLV	61	LLQRPQGSPRRLIYLV	120
Qy	121	RTFGGGTKLEIK	121	RTFGGGTKLEIK	132
Db	121	YTFGGGGTKLVIK	121	YTFGGGGTKLVIK	132

Search completed: December 13, 2004, 19:13:22  
Job time : 113.978 secs

OM protein - protein search, using sw model

Run on: December 13, 2004, 19:05:17 ; Search time 27.3778 Seconds  
 (without alignments)  
 319.748 Million cell updates/sec

Title: US-10-010-942B-2  
 Perfect score: 692  
 Sequence: 1 MMSPAQFLFLLVLWIRETNG.....CWQGTHTFPRTFGGGTKLEIK 132

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
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 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

8						
Result	Query					
No.	Score	Match	Length	DB	ID	Description
1	649	93.8	131	4	US-09-647-468-163	Sequence 163, App
2	646	93.4	131	4	US-09-647-468-164	Sequence 164, App
3	606	87.6	142	4	US-09-840-459-102	Sequence 102, App
4	606	87.6	142	4	US-09-497-625A-102	Sequence 102, App
5	562	81.2	353	4	US-09-203-958A-4	Sequence 4, Appli
6	560	80.9	112	4	US-09-809-739-11	Sequence 11, Appl
7	560	80.9	112	4	US-09-840-459-9	Sequence 9, Appli
8	560	80.9	112	4	US-09-497-625A-9	Sequence 9, Appli
9	559	80.8	112	4	US-09-647-468-149	Sequence 149, App
10	559	80.8	112	4	US-09-647-468-150	Sequence 150, App
11	556	80.3	112	4	US-09-840-459-54	Sequence 54, Appl

12	556	80.3	112	4	US-09-497-625A-54	Sequence 54, Appl
13	548	79.2	112	2	US-08-678-194-6	Sequence 6, Appli
14	548	79.2	112	3	US-08-890-011-6	Sequence 6, Appli
15	548	79.2	112	3	US-09-262-724-6	Sequence 6, Appli
16	548	79.2	535	3	US-08-983-035A-38	Sequence 38, Appl
17	538	77.7	112	4	US-09-809-739-16	Sequence 16, Appl
18	538	77.7	112	4	US-09-840-459-14	Sequence 14, Appl
19	538	77.7	112	4	US-09-497-625A-14	Sequence 14, Appl
20	537	77.6	132	1	US-08-477-877B-91	Sequence 91, Appl
21	537	77.6	132	2	US-08-472-281A-91	Sequence 91, Appl
22	537	77.6	132	2	US-08-477-989B-91	Sequence 91, Appl
23	533	77.0	112	4	US-09-809-739-17	Sequence 17, Appl
24	533	77.0	112	4	US-09-840-459-15	Sequence 15, Appl
25	533	77.0	112	4	US-09-497-625A-15	Sequence 15, Appl
26	530	76.6	112	4	US-09-809-739-15	Sequence 15, Appl
27	530	76.6	112	4	US-09-840-459-13	Sequence 13, Appl
28	530	76.6	112	4	US-09-497-625A-13	Sequence 13, Appl
29	527	76.2	114	4	US-09-840-459-106	Sequence 106, App
30	527	76.2	114	4	US-09-497-625A-106	Sequence 106, App
31	525	75.9	112	4	US-09-809-739-18	Sequence 18, Appl
32	525	75.9	112	4	US-09-840-459-107	Sequence 107, App
33	520	75.1	112	4	US-09-809-739-14	Sequence 14, Appl
34	520	75.1	112	4	US-09-840-459-12	Sequence 12, Appl
35	520	75.1	112	4	US-09-497-625A-12	Sequence 12, Appl
36	518	74.9	132	1	US-08-477-877B-84	Sequence 84, Appl
37	518	74.9	132	2	US-08-472-281A-84	Sequence 84, Appl
38	518	74.9	132	2	US-08-477-989B-84	Sequence 84, Appl
39	515	74.4	100	4	US-09-840-459-22	Sequence 22, Appl
40	515	74.4	100	4	US-09-497-625A-22	Sequence 22, Appl
41	515	74.4	135	1	US-08-259-372A-12	Sequence 12, Appl
42	515	74.4	135	1	US-08-468-671-12	Sequence 12, Appl
43	512	74.0	112	3	US-09-184-658-49	Sequence 49, Appl
44	512	74.0	112	4	US-09-504-262D-49	Sequence 49, Appl
45	508	73.4	289	3	US-09-184-658-63	Sequence 63, Appl

#### ALIGNMENTS

##### RESULT 1

US-09-647-468-163

; Sequence 163, Application US/09647468

; Patent No. 6677436

; GENERAL INFORMATION:

; APPLICANT: SATO, KOH

; APPLICANT: ADACHI, HIDEKI

; APPLICANT: YABUTA, NAOHIRO

; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND

; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY

; FILE REFERENCE: 053466/0289

; CURRENT APPLICATION NUMBER: US/09/647,468

; CURRENT FILING DATE: 2000-09-29

; PRIOR APPLICATION NUMBER: PCT/JP99/01768

; PRIOR FILING DATE: 1999-04-02

; PRIOR APPLICATION NUMBER: JP 10-91850

; PRIOR FILING DATE: 1998-04-03

; NUMBER OF SEQ ID NOS: 183

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 163
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence coding for L chain V region of ant-TF
; OTHER INFORMATION: mouse monoclonal antibody ATR-7
US-09-647-468-163
```

```
Query Match          93.8%; Score 649; DB 4; Length 131;
Best Local Similarity 93.9%; Pred. No. 5.4e-55;
Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      2 MSPAQFLFLLVLWIRETNGYVVMQTPTLTLSTIGQPASISCKSSQSLLSDGKTYLNWL 61
        |||||
Db      1 MSPAQFLFLLVLWIREINGDVVLTQTPTLTLSTIGQPASVSCKSSQSLLSDGKTYLNWL 60

Qy      62 LQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGFHPR 121
        |||||
Db      61 LQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQDTHFPD 120

Qy      122 TFGGGTKLEIK 132
        |||||
Db      121 TFGGGTKLEIK 131
```

# RESULT 2

```
US-09-647-468-164
; Sequence 164, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NAOHIRO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 164
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence coding for L chain V region of ant-TF
; OTHER INFORMATION: mouse monoclonal antibody ATR-8
US-09-647-468-164
```

Query Match 93.4%; Score 646; DB 4; Length 131;  
Best Local Similarity 93.1%; Pred. No. 1e-54;  
Matches 122; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

```
Qy      2 MSPAQFLFLLVLWIRETNGYVVMQTPTLTLSTIGQPASISCKSSQSLLDSDGKTYLNWL 61
      |||||||||||||: || ||:|||||||||||||||:|||||||||||||||
Db      1 MSPAQFLFLLVLWIRDINGDVVLTQTPTLTLSTIGQPASVSCSSQSLLDSDGKTYLNWL 60

Qy     62 LQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPR 121
      |||||||||||||||||||||||||||||||||||||:|||||:||||| |||
Db     61 LQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGYYCWQDTHFPD 120

Qy    122 TFGGGTKLEIK 132
      |||||||||
Db    121 TFGGGTKLEIK 131
```

RESULT 3

US-09-840-459-102

; Sequence 102, Application US/09840459

; Patent No. 6696550

; GENERAL INFORMATION:

; APPLICANT: LaRosa, Gregory J.

; APPLICANT: Horvath, Christopher

; APPLICANT: Newman, Walter

; APPLICANT: Jones, S. Tarran

; APPLICANT: O'Brien, Siobhan H.

; APPLICANT: O'Keefe, Theresa

; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND

; TITLE OF INVENTION: METHODS OF USE THEREFOR

; FILE REFERENCE: 1855.1052-012

; CURRENT APPLICATION NUMBER: US/09/840,459

; CURRENT FILING DATE: 2001-02-02

; PRIOR APPLICATION NUMBER: PCT/US01/03537

; PRIOR FILING DATE: 2001-02-02

; PRIOR APPLICATION NUMBER: 09/497,625

; PRIOR FILING DATE: 2000-02-03

; PRIOR APPLICATION NUMBER: 09/359,193

; PRIOR FILING DATE: 1999-07-22

; PRIOR APPLICATION NUMBER: 09/121,781

; PRIOR FILING DATE: 1998-07-23

; NUMBER OF SEQ ID NOS: 107

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 102

; LENGTH: 142

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-840-459-102

Query Match 87.6%; Score 606; DB 4; Length 142;  
Best Local Similarity 93.5%; Pred. No. 7.8e-51;  
Matches 115; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

```
Qy      10 LLVLWIRETNGYVVMQTPTLTLSTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPQGSP 69
      ||||||| | |||||||||||||:| |||||||||||||||||||:|||||||
Db      7 LLVLWIRETIGDVVMTQTPTLTLSTVGHAPASISCKSSQSLLDSDGKTFLNWLLQRPQGSP 66
```

Qy 70 KRLIYLVSKLD SGVPDRFTGSGSGTDFTLKISR IEAEDLGLYYCWQGTHFPRTFGGGTKL 129  
 |||  
 Db 67 KRLIYLVSKLD SGVPDRFTGSGSGTDFTLKISRVEAEDLG VYYCWQGTHFPYTFGGGTKL 126

Qy 130 EIK 132  
 |||  
 Db 127 EIK 129

#### RESULT 4

US-09-497-625A-102  
 ; Sequence 102, Application US/09497625A  
 ; Patent No. 6727349  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LaRosa, Gregory J.  
 ; APPLICANT: Horvath, Christopher  
 ; APPLICANT: Newman, Walter  
 ; APPLICANT: Jones, S. Tarran  
 ; APPLICANT: O'Brien, Siobhan H.  
 ; APPLICANT: O'Keefe, Theresa  
 ; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
 ; TITLE OF INVENTION: METHODS OF USE THEREFOR  
 ; FILE REFERENCE: 1855.1052-004  
 ; CURRENT APPLICATION NUMBER: US/09/497,625A  
 ; CURRENT FILING DATE: 2000-02-03  
 ; PRIOR APPLICATION NUMBER: 09/359,193  
 ; PRIOR FILING DATE: 1999-07-22  
 ; PRIOR APPLICATION NUMBER: 09/121,781  
 ; PRIOR FILING DATE: 1998-07-23  
 ; NUMBER OF SEQ ID NOS: 106  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO 102  
 ; LENGTH: 142  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-09-497-625A-102

Query Match 87.6%; Score 606; DB 4; Length 142;  
 Best Local Similarity 93.5%; Pred. No. 7.8e-51;  
 Matches 115; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 10 LLVLWIRETNGYVVM TQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSP 69  
 |||  
 Db 7 LLVLWIRETIGDVVM TQTPLTSLVTVGH PASISCKSSQSLDSDGKTFLNWLLQRPQGSP 66

Qy 70 KRLIYLVSKLD SGVPDRFTGSGSGTDFTLKISR IEAEDLGLYYCWQGTHFPRTFGGGTKL 129  
 |||  
 Db 67 KRLIYLVSKLD SGVPDRFTGSGSGTDFTLKISRVEAEDLG VYYCWQGTHFPYTFGGGTKL 126

Qy 130 EIK 132  
 |||  
 Db 127 EIK 129

#### RESULT 5

US-09-203-958A-4  
 ; Sequence 4, Application US/09203958A



```
; Patent No. 6682928
; GENERAL INFORMATION:
; APPLICANT: KELER, Tibor
; APPLICANT: GOLDSTEIN, Joel
; APPLICANT: GRAZIANO, Robert
; APPLICANT: DEO, Yashwant M.
; TITLE OF INVENTION: CELLS EXPRESSING ANTI-FC RECEPTOR
; TITLE OF INVENTION: BINDING COMPONENTS
; FILE REFERENCE: MXI-099CPA
; CURRENT APPLICATION NUMBER: US/09/203,958A
; CURRENT FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 60/067232
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-203-958A-4
```

```
Query Match          81.2%; Score 562; DB 4; Length 353;
Best Local Similarity 94.6%; Pred. No. 3.7e-46;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      22 VVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
          |||||:|||||
Db      177 VVMTQTPLTSLITIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPTRLIYLVSKLDS 236

Qy      82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTTFPRTFGGGTKLEIK 132
          |||||:|||||
Db      237 GVPDRFTGSGSGTDFTLKISRVEAEDLGIYYCWQGAHFPQTFGGGTKLEIK 287
```

# RESULT 6

US-09-809-739-11

```
; Sequence 11, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
```

```

; NAME/KEY: SITE
; LOCATION: (1)...(112)
; OTHER INFORMATION: Murine mAb 1D9 light chain variable region
; NAME/KEY: SITE
; LOCATION: (24)...(39)
; OTHER INFORMATION: CDR1
; NAME/KEY: SITE
; LOCATION: (55)...(61)
; OTHER INFORMATION: CDR2
; NAME/KEY: SITE
; LOCATION: (94)...(102)
; OTHER INFORMATION: CDR3
; OTHER INFORMATION: Mouse
US-09-809-739-11

```

```

Query Match          80.9%;  Score 560;  DB 4;  Length 112;
Best Local Similarity 94.6%;  Pred. No. 1.5e-46;
Matches 105;  Conservative 4;  Mismatches 2;  Indels 0;  Gaps 0;

```

```

Qy      22 VVMTQTPLTSLVTIGQPASISCKSSQSLLDSGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
          |||||:| |||||:|||||
Db      2  VVMTQTPLTSLVTVGHPASISCKSSQSLLDSGKTFLNWLLQRPQGSPKRLIYLVSKLDS 61

Qy      82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGFHFPRTFGGGTKLEIK 132
          |||||:|||||:||||| |||||
Db      62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGFHFPYTFGGGTKLEIK 112

```

# RESULT 7

```

US-09-840-459-9
; Sequence 9, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 112
; TYPE: PRT

```

; ORGANISM: Mus musculus  
US-09-840-459-9

Query Match 80.9%; Score 560; DB 4; Length 112;  
Best Local Similarity 94.6%; Pred. No. 1.5e-46;  
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81  
| | | | | : | | | | | : | | | | |  
Db 2 VVMTQTPLTSLVTVGHPPASISCKSSQSLDSDGKTFLNWLLQRPQGSPKRLIYLVSKLDS 61  
  
Qy 82 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHTFPRTFGGGTKLEIK 132  
| | | | | : | | | | | : | | | | |  
Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHTFPYTFGGGTKLEIK 112

RESULT 8

US-09-497-625A-9

; Sequence 9, Application US/09497625A  
; Patent No. 6727349  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; TITLE OF INVENTION: METHODS OF USE THEREFOR  
; FILE REFERENCE: 1855.1052-004  
; CURRENT APPLICATION NUMBER: US/09/497,625A  
; CURRENT FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 106  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 9  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-497-625A-9

Query Match 80.9%; Score 560; DB 4; Length 112;  
Best Local Similarity 94.6%; Pred. No. 1.5e-46;  
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81  
| | | | | : | | | | | : | | | | |  
Db 2 VVMTQTPLTSLVTVGHPPASISCKSSQSLDSDGKTFLNWLLQRPQGSPKRLIYLVSKLDS 61  
  
Qy 82 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHTFPRTFGGGTKLEIK 132  
| | | | | : | | | | | : | | | | |  
Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHTFPYTFGGGTKLEIK 112

# RESULT 9

US-09-647-468-149

; Sequence 149, Application US/09647468

; Patent No. 6677436

; GENERAL INFORMATION:

; APPLICANT: SATO, KOH

; APPLICANT: ADACHI, HIDEKI

; APPLICANT: YABUTA, NAOHIRO

; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND

; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY

; FILE REFERENCE: 053466/0289

; CURRENT APPLICATION NUMBER: US/09/647,468

; CURRENT FILING DATE: 2000-09-29

; PRIOR APPLICATION NUMBER: PCT/JP99/01768

; PRIOR FILING DATE: 1999-04-02

; PRIOR APPLICATION NUMBER: JP 10-91850

; PRIOR FILING DATE: 1998-04-03

; NUMBER OF SEQ ID NOS: 183

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 149

; LENGTH: 112

; TYPE: PRT

; ORGANISM: Mus sp.

; FEATURE:

; OTHER INFORMATION: Amino acid sequence of L chain V region of anti-TF mouse

; OTHER INFORMATION: monoclonal antibody ATR-7

US-09-647-468-149

Query Match 80.8%; Score 559; DB 4; Length 112;

Best Local Similarity 94.6%; Pred. No. 1.9e-46;

Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81

||:||||||||||||||:||||||||||||||||||||||||||||||||||||||

Db 2 VVLTQTPLTSLVTIGQPASVCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 61

Qy 82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTDFPRTFGGGTKLEIK 132

||||||||||||||||||:|||||:||||| |||| |||||||||

Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQDTHFPDFTFGGGTKLEIK 112

# RESULT 10

US-09-647-468-150

; Sequence 150, Application US/09647468

; Patent No. 6677436

; GENERAL INFORMATION:

; APPLICANT: SATO, KOH

; APPLICANT: ADACHI, HIDEKI

; APPLICANT: YABUTA, NAOHIRO

; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND

; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY

; FILE REFERENCE: 053466/0289

; CURRENT APPLICATION NUMBER: US/09/647,468

; CURRENT FILING DATE: 2000-09-29

; PRIOR APPLICATION NUMBER: PCT/JP99/01768

; PRIOR FILING DATE: 1999-04-02

; PRIOR APPLICATION NUMBER: JP 10-91850

; PRIOR FILING DATE: 1998-04-03  
; NUMBER OF SEQ ID NOS: 183  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 150  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Mus sp.  
; FEATURE:  
; OTHER INFORMATION: Amino acid sequence of L chain V region of anti-TF mouse  
; OTHER INFORMATION: monoclonal antibody ATR-8  
US-09-647-468-150

Query Match 80.8%; Score 559; DB 4; Length 112;  
Best Local Similarity 94.6%; Pred. No. 1.9e-46;  
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 81  
||:||||||||||||||:||||||||||||||||||||||||||||||||||  
Db 2 VVLTQTPLTSLVTIGQPASVSKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 61  
  
Qy 82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTDFPRTFGGGTKLEIK 132  
||||||||||||||||||:|||||:||||| |||| |||||||||  
Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQDTHFPDFTFGGGTKLEIK 112

#### RESULT 11

US-09-840-459-54  
; Sequence 54, Application US/09840459  
; Patent No. 6696550  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; TITLE OF INVENTION: METHODS OF USE THEREFOR  
; FILE REFERENCE: 1855.1052-012  
; CURRENT APPLICATION NUMBER: US/09/840,459  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: PCT/US01/03537  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/497,625  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 54  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-840-459-54

Query Match 80.3%; Score 556; DB 4; Length 112;  
Best Local Similarity 92.8%; Pred. No. 3.7e-46;  
Matches 103; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

```
Qy      22 VVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
          : :||:|||||
Db      2  IQLTQSPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 61

Qy      82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTTHFPRTFGGGTKLEIK 132
          |||||
Db      62 GVPDRFTGSGSGTDFTLKISRVEADDLGVYYCWQGTTHFPQTFGGGTKLEIK 112
```

RESULT 12

US-09-497-625A-54

; Sequence 54, Application US/09497625A

; Patent No. 6727349

; GENERAL INFORMATION:

; APPLICANT: LaRosa, Gregory J.

; APPLICANT: Horvath, Christopher

; APPLICANT: Newman, Walter

; APPLICANT: Jones, S. Tarran

; APPLICANT: O'Brien, Siobhan H.

; APPLICANT: O'Keefe, Theresa

; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND

; TITLE OF INVENTION: METHODS OF USE THEREFOR

; FILE REFERENCE: 1855.1052-004

; CURRENT APPLICATION NUMBER: US/09/497,625A

; CURRENT FILING DATE: 2000-02-03

; PRIOR APPLICATION NUMBER: 09/359,193

; PRIOR FILING DATE: 1999-07-22

; PRIOR APPLICATION NUMBER: 09/121,781

; PRIOR FILING DATE: 1998-07-23

; NUMBER OF SEQ ID NOS: 106

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 54

; LENGTH: 112

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-497-625A-54

Query Match 80.3%; Score 556; DB 4; Length 112;  
Best Local Similarity 92.8%; Pred. No. 3.7e-46;  
Matches 103; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

```
Qy      22 VVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
          : :||:|||||
Db      2  IQLTQSPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 61

Qy      82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTTHFPRTFGGGTKLEIK 132
          |||||
Db      62 GVPDRFTGSGSGTDFTLKISRVEADDLGVYYCWQGTTHFPQTFGGGTKLEIK 112
```

RESULT 13

US-08-678-194-6

; Sequence 6, Application US/08678194

```

; Patent No. 5922845
; GENERAL INFORMATION:
; APPLICANT: Deo, Yashwant M.
; APPLICANT: Graziano, Robert
; APPLICANT: Keler, Tibor
; TITLE OF INVENTION: Therapeutic Multispecific Compounds
; TITLE OF INVENTION: Comprised of Anti-Fc{SYMBOL 97 \f "Symbol"} Receptor
Antibodi
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/678,194
; FILING DATE: July 11, 1996
; PRIOR APPLICATION DATA: No. 5922845e
; APPLICATION NUMBER: US
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Beth A. Arnold
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-678-194-6

```

```

Query Match          79.2%; Score 548; DB 2; Length 112;
Best Local Similarity 91.0%; Pred. No. 2.2e-45;
Matches 101; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

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Qy      22 VVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLWLLQRPQGSPKRLIYLVSKLDS 81
          : :||:||||:|||||||||||||||||||||||||||||||||||||
Db      2 IQLTQSPLTSLITIGQPASISCKSSQSLDSDGKTYLWLLQRPQSPTRLIYLVSKLDS 61

Qy      82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHTFPRTFGGGTKLEIK 132
          ||||||||||||||||:|||||:||||| |||:|||||||
Db      62 GVPDRFTGSGSGTDFTLKISRVEAEDLGIYYCWQGAHFPQTFGGGTKLEIK 112

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RESULT 14
US-08-890-011-6

```

```

; Sequence 6, Application US/08890011
; Patent No. 6193966
; GENERAL INFORMATION:
; APPLICANT: Deo, Yashwant M.
; APPLICANT: Graziano, Robert
; APPLICANT: Keler, Tibor
; TITLE OF INVENTION: Therapeutic Multispecific Compounds
; TITLE OF INVENTION: Comprised of Anti-Fc
; TITLE OF INVENTION: {SYMBOL 97 \f "Symbol"} Receptor Antibodies
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,011
; FILING DATE: July 9, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/678,194
; FILING DATE: July 11, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane E. Remillard
; REGISTRATION NUMBER: 38,872
; REFERENCE/DOCKET NUMBER: MXI-064CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-890-011-6

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Query Match          79.2%; Score 548; DB 3; Length 112;
Best Local Similarity 91.0%; Pred. No. 2.2e-45;
Matches 101; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

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```

Qy      22 VVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
          : :||:||||:|||||||||||||||||||||||||||||||||||||
Db      2 IQLTQSPLTSLITIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPTRLIYLVSKLDS 61

Qy      82 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
          ||||||||||||||||||||:|||||:||||| |||:|||||
Db      62 GVPDRFTGSGSGTDFTLKISRVEAEDLGIYYCWQGAHFPQTFGGGTKLEIK 112

```

RESULT 15



US-09-262-724-6

; Sequence 6, Application US/09262724  
; Patent No. 6303755

; GENERAL INFORMATION:

; APPLICANT: Deo, Yashwant M.  
; Graziano, Robert  
; Keler, Tibor

; TITLE OF INVENTION: Therapeutic Multispecific Compounds  
; Comprised of Anti-Fc{SYMBOL 97 \f "Symbol"}  
; Receptor Antibodies

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street, Suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/262,724  
; FILING DATE: 04-Mar-1999

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/678,194  
; FILING DATE: July 11, 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Beth A. Arnold  
; REGISTRATION NUMBER: 35,430  
; REFERENCE/DOCKET NUMBER: MXI-064

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 112 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-262-724-6

Query Match 79.2%; Score 548; DB 3; Length 112;  
Best Local Similarity 91.0%; Pred. No. 2.2e-45;  
Matches 101; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 22 VMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 81  
: :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 2 IQLTQSPLTSLITIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPTRLIYLVSKLDS 61  
  
Qy 82 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGAHFPQTFTGGGKLEIK 132  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGAHFPQTFTGGGKLEIK 112

Search completed: December 13, 2004, 19:19:40  
Job time : 28.3778 secs

OM protein - protein search, using sw model

Run on: December 13, 2004, 19:04:43 ; Search time 23.4667 Seconds  
 (without alignments)  
 541.219 Million cell updates/sec

Title: US-10-010-942B-2  
 Perfect score: 692  
 Sequence: 1 MMSPAQFLFLVLWIRETNG.....CWQGTHTFPRTFGGGTKLEIK 132

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : PIR\_79:\*  
 1: pir1:\*  
 2: pir2:\*  
 3: pir3:\*  
 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	678	98.0	132	2	C32513	Ig kappa chain pre
2	587	84.8	131	2	S31577	Ig kappa chain m
3	566	81.8	113	2	F30560	Ig kappa chain V r
4	554	80.1	112	2	A55491	proteolytic antibo
5	548	79.2	112	2	A36259	ig kappa chain V r
6	547	79.0	111	2	S20709	Ig kappa chain V r
7	536	77.5	112	2	PL0273	Ig kappa chain V r
8	516	74.6	133	2	S42611	HUNVK protein prec
9	515	74.4	101	2	A33730	Ig kappa chain V r
10	515	74.4	133	2	S23230	Ig kappa chain pre
11	513	74.1	142	2	S22902	Ig kappa chain V r
12	512	74.0	133	2	S40324	Ig kappa chain V r
13	508	73.4	133	1	K2HURP	Ig kappa chain pre

14	502.5	72.6	140	2	S22658	Ig kappa chain pre
15	496	71.7	133	1	A24452	Ig kappa chain pre
16	491	71.0	132	2	S40322	Ig kappa chain - h
17	485	70.1	103	2	PH1055	Ig light chain V r
18	476	68.8	91	2	S42186	Ig kappa chain V r
19	473	68.4	120	2	S42268	Ig kappa chain V r
20	473	68.4	120	2	S42267	Ig kappa chain V r
21	470	67.9	131	2	S09259	Ig kappa chain pre
22	466	67.3	103	2	PH1056	Ig light chain V r
23	463	66.9	126	2	S40312	Ig kappa chain - h
24	463	66.9	131	2	D29380	Ig kappa chain pre
25	462.5	66.8	131	2	S40355	Ig kappa chain - h
26	462	66.8	132	2	S26882	Ig kappa chain V r
27	461.5	66.7	114	2	S49572	Ig kappa chain pre
28	460	66.5	118	2	S40374	Ig kappa chain - h
29	458.5	66.3	114	2	B49002	Ig kappa chain V r
30	458	66.2	131	2	B34904	Ig kappa chain pre
31	458	66.2	136	2	S40357	Ig kappa chain V-J
32	456	65.9	112	2	A31807	Ig kappa chain V r
33	456	65.9	131	2	B39276	Ig light chain pre
34	455	65.8	132	2	PH0106	anti-digoxin trans
35	454	65.6	131	2	C34904	Ig kappa chain pre
36	452.5	65.4	134	2	S40376	Ig kappa chain - h
37	452	65.3	122	2	S40338	Ig kappa chain - h
38	451	65.2	128	2	S40373	Ig kappa chain - h
39	450.5	65.1	130	2	S40321	Ig kappa chain - h
40	450	65.0	131	2	D34904	Ig kappa chain pre
41	450	65.0	131	2	B30577	Ig kappa chain pre
42	448	64.7	131	2	G34903	Ig kappa chain pre
43	448	64.7	135	2	S40342	Ig kappa chain - h
44	447	64.6	131	2	B32513	Ig kappa chain pre
45	446	64.5	115	2	S38715	Ig kappa chain V r

# ALIGNMENTS

## RESULT 1

C32513

Ig kappa chain precursor V region (BXW14) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 21-May-1990 #sequence\_revision 31-Dec-1990 #text\_change 21-Jan-2000

C;Accession: C32513

R;Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.;

Duchosal, M.A.; Dixon, F.J.; Theofilopoulos, A.N.

J. Clin. Invest. 82, 852-860, 1988

A;Title: Immunoglobulin kappa light chain variable region gene complex organization and immunoglobulin genes encoding anti-DNA autoantibodies in lupus mice.

A;Reference number: A94689; MUID:88331394; PMID:3138286

A;Accession: C32513

A;Molecule type: DNA

A;Residues: 1-132 <KOF>

A;Cross-references: GB:M20830; NID:g196939; PIDN:AAA38844.1; PID:g196940

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;36-115/Domain: immunoglobulin homology <IMM>

Query Match 98.0%; Score 678; DB 2; Length 132;  
Best Local Similarity 97.7%; Pred. No. 1.6e-51;  
Matches 129; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNW 60
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 MMSPAQFLFLLVLWIRETNGDVVMTQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNW 60

Qy      61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFP 120

Qy      121 RTFGGGTKLEIK 132
        |||||:|||||
Db      121 RTFGGGTKLEIK 132
```

## RESULT 2

S31577

Ig kappa chain - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000

C;Accession: S31577

R;Recinos, A.; Silvey, K.J.; Jensen, R.H.; Stanker, L.H.

submitted to the EMBL Data Library, January 1993

A;Description: Immunoglobulin variable heavy and light chain cDNA sequences for two antidioxin monoclonals.

A;Reference number: S31577

A;Accession: S31577

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-131 <REC>

A;Cross-references: EMBL:Z19575; NID:g53983; PIDN:CAA79627.1; PID:g53984

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 84.8%; Score 587; DB 2; Length 131;  
Best Local Similarity 86.3%; Pred. No. 1.1e-43;  
Matches 113; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

```
Qy      2 MSPAQFLFLLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNWL 61
        |||||:|| | |:| || |||||:|||||:|||||:|||||:|||||
Db      1 MSPAQFLFLLVLSIQEINGDVVMTQAPLTSLVTLGQPASISCKSSHLLSIDGKTYLNWL 60

Qy      62 LQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPR 121
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 LQRPQGSPKRLIYLVSKLDSGVPDRFSGSGSGTDFTLRISRVEAEDLGVYYCMQNTHTFPY 120

Qy      122 TFGGGTKLEIK 132
        |||||:|||||
Db      121 TFGGGTKLEMK 131
```

## RESULT 3

F30560

Ig kappa chain V region (28.4.10A) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 23-Mar-1989 #sequence\_revision 23-Mar-1989 #text\_change 21-Jan-2000  
 C;Accession: F30560  
 R;Matsuda, T.; Kabat, E.A.  
 J. Immunol. 142, 863-870, 1989  
 A;Title: Variable region cDNA sequences and antigen binding specificity of mouse monoclonal antibodies to isomaltosyl oligosaccharides coupled to proteins. T-dependent analogues of alpha(1->6)dextran.  
 A;Reference number: A30560; MUID:89110062; PMID:2464028  
 A;Accession: F30560  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-113 <MAT>  
 A;Cross-references: GB:M24273; NID:g197081; PIDN:AAA63370.1; PID:g197082  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 81.8%; Score 566; DB 2; Length 113;  
 Best Local Similarity 96.4%; Pred. No. 6e-42;  
 Matches 107; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

Qy      22 VVMTQTPLTSLVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
        ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2  VVMTQIPLTSLVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 61

Qy      82 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHTFPRTFGGGTKLEIK 132
        ||||||||||||||||:|||||:||||||| |||||||||
Db      62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHTFPHTFGGGTKLEIK 112
  
```

#### RESULT 4

A55491  
 proteolytic antibody light chain - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 03-Mar-1995 #sequence\_revision 03-Mar-1995 #text\_change 09-Jul-2004  
 C;Accession: A55491  
 R;Gao, Q.S.; Sun, M.; Tyutyulkova, S.; Webster, D.; Rees, A.; Tramontano, A.; Massey, R.J.; Paul, S.  
 J. Biol. Chem. 269, 32389-32393, 1994  
 A;Title: Molecular cloning of a proteolytic antibody light chain.  
 A;Reference number: A55491; MUID:95096089; PMID:7798238  
 A;Accession: A55491  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-112 <GAO>  
 A;Cross-references: UNIPROT:Q8K0F8; GB:L34775  
 A;Note: authors translated the codon TAT for residue 37 as Thr  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 80.1%; Score 554; DB 2; Length 112;  
 Best Local Similarity 94.6%; Pred. No. 6.4e-41;  
 Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

```

Qy      22 VVMTQTPLTSLVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
  
```

```

      |||
Db      2 VVMTQTPLTSLVTIGQPASISCKSSQSLHLDGKTYLIWLLQRPQGSPKRLIYLVSKLDS 61

Qy      82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
      |||
Db      62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPQTFGGGTKLEIK 112

```

# RESULT 5

A36259  
 ig kappa chain V region (TE34) - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 18-Jan-1991 #sequence\_revision 18-Jan-1991 #text\_change 21-Jan-2000  
 C;Accession: A36259  
 R;Zilber, B.; Scherf, T.; Levitt, M.; Anglister, J.  
 Biochemistry 29, 10032-10041, 1990  
 A;Title: NMR-derived model for a peptide-antibody complex.  
 A;Reference number: A36259; MUID:91104915; PMID:2271636  
 A;Accession: A36259  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-112 <ZIL>  
 A;Cross-references: GB:M30458; GB:M30459; GB:M30480; GB:M30481; GB:M30482;  
 GB:M30483  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;16-95/Domain: immunoglobulin homology <IMM>

```

Query Match          79.2%; Score 548; DB 2; Length 112;
Best Local Similarity 94.6%; Pred. No. 2.1e-40;
Matches 105; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```

```

Qy      22 VVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
      |||
Db      2 VVMIQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 61

Qy      82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
      |||
Db      62 GVPTRFTGSGSGTDFTLKISRVEAEDGGVYYCWQGTHFPWTFGGGTKLEIK 112

```

# RESULT 6

S20709  
 Ig kappa chain V region - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000  
 C;Accession: S20709  
 R;Brennand, D.M.; Hinds, M.G.; Welsh, J.H.; Tempest, P.R.; Harris, W.J.; Carr,  
 F.J.; Osborn, N.J.; Glennie, M.J.; Richards, N.G.; Robinson, J.A.  
 submitted to the EMBL Data Library, April 1992  
 A;Description: Binding specificity and variable region sequences of two  
 monoclonal antibodies that recognise a beta-turn forming peptide containing  
 alpha-methylproline.  
 A;Reference number: S20706  
 A;Accession: S20709  
 A;Status: preliminary  
 A;Molecule type: DNA

A;Residues: 1-111 <BRE>  
A;Cross-references: EMBL:Z11917; NID:g52655; PIDN:CAA77975.1; PID:g52656  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 547; DB 2; Length 111;  
Best Local Similarity 92.7%; Pred. No. 2.5e-40;  
Matches 102; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81  
: :||:||||||||||||||||||||| |||||||||||||||||||||||  
Db 2 IQLTQSPLTSLVTIGQPASISCKSSQSLLHSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 61  
  
Qy 82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTFGGGTKLEI 131  
||||||||||||||||||:|||||:|||||||:|||||||  
Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPQTFGGGTKLEI 111

#### RESULT 7

PL0273

Ig kappa chain V region (anti-DNA, D23VK) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 09-Jul-2004

C;Accession: PL0273

R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.; Weigert, M.

J. Exp. Med. 171, 265-297, 1990

A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic mutation.

A;Reference number: PL0231; MUID:90111618; PMID:2104919

A;Accession: PL0273

A;Molecule type: mRNA

A;Residues: 1-112 <SHL>

A;Cross-references: UNIPROT:Q8K0F8

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-23/Region: framework 1

F;16-95/Domain: immunoglobulin homology <IMM>

F;24-39/Region: complementarity-determining 1

F;40-54/Region: framework 2

F;55-61/Region: complementarity-determining 2

F;62-93/Region: framework 3

F;94-102/Region: complementarity-determining 3

F;103-112/Region: framework 4

Query Match 77.5%; Score 536; DB 2; Length 112;  
Best Local Similarity 93.7%; Pred. No. 2.3e-39;  
Matches 104; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81  
||||||||||||||||||||| :|||||||||||||||||||||  
Db 2 VVMTQTPLTSLVTIGQPASISCKSSQSLLYRNGKTYLNWLLQRPQGSPKRLIYLVSKLDS 61  
  
Qy 82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132  
||||||||||||||||||:|||||:||| ||||| |||||||||  
Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCVQGTHFPWTFGGGTKLEIK 112



RESULT 8

S42611

HUNVK protein precursor - human

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jan-2000

C;Accession: S42611

R;Spatz, L.A.; Williams, M.; Brender, B.; Desai, R.; Latov, N.

J. Neuroimmunol. 36, 29-39, 1992

A;Title: DNA sequence analysis and comparison of the variable heavy and light chain regions of two IgM, monoclonal, anti-myelin associated glycoprotein antibodies.

A;Reference number: S42610; MUID:92138794; PMID:1370957

A;Accession: S42611

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-133 <SPA>

A;Cross-references: EMBL:X54137; NID:g433889; PIDN:CAA38072.1; PID:g433890

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;36-115/Domain: immunoglobulin homology <IMM>

Query Match 74.6%; Score 516; DB 2; Length 133;  
Best Local Similarity 74.0%; Pred. No. 1.4e-37;  
Matches 97; Conservative 16; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNW 60  
| ||| | ||:||: ::| ||||:|:| ||:|||||:||||: ||| |||||  
Db 1 MRLPAQLLGLLMLWVPGSSGDVMTQSPSLPVTLGQPASISCRSSQSLVFS DGNTYLNW 60

Qy 61 LLQRPQGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISR IEAEDLGLYYCWQGT HFP 120  
|||||:|||| || |||||:||||| |||||:||||: || ||:|  
Db 61 FQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGTDFTLKISRVEAEDVGIYYCMQGAHWP 120

Qy 121 RTFGGGTKLEI 131  
|||||:||  
Db 121 LTFGGGTKVEI 131

RESULT 9

A33730

Ig kappa chain V region (1.60) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 09-Mar-1990 #sequence\_revision 18-Sep-1992 #text\_change 21-Jan-2000

C;Accession: A33730

R;Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.

Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989

A;Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, unlike genes encoding heavy chains, use variable gene segments dispersed throughout the locus.

A;Reference number: A33730; MUID:89367325; PMID:2505260

A;Accession: A33730

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-101 <LAW>

A;Cross-references: GB:M25996; NID:g197109; PIDN:AAA38911.1; PID:g197110

A;Note: the authors translated the codon CGC for residue 51 as Leu, and TTG for residue 88 as Phe

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 74.4%; Score 515; DB 2; Length 101;  
Best Local Similarity 98.0%; Pred. No. 1.3e-37;  
Matches 97; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy      22 VVMTQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
          |||
Db      2 VVMTQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 61

Qy      82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
          |||
Db      62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFP 100
```

#### RESULT 10

S23230

Ig kappa chain precursor V-J region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jan-2000

C;Accession: S23230

R;Kennedy, M.A.

J. Exp. Med. 173, 1033-1036, 1991

A;Title: Novel chromosome translocation caused by fusion of immunoglobulin heavy and light chain V genes in a human B lymphoblastoid cell line.

A;Reference number: S23230; MUID:91178438; PMID:1840606

A;Accession: S23230

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-133 <KEN>

A;Cross-references: EMBL:X55400; NID:g33999; PIDN:CAA39072.1; PID:g34000

C;Genetics:

A;Introns: 17/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;36-115/Domain: immunoglobulin homology <IMM>

Query Match 74.4%; Score 515; DB 2; Length 133;  
Best Local Similarity 74.2%; Pred. No. 1.7e-37;  
Matches 98; Conservative 16; Mismatches 18; Indels 0; Gaps 0;

```
Qy      1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNW 60
          | ||| | ||:|: :|| ||||:|:| ||:|||||:||||: ||| |:|
Db      1 MRLPAQLLGLLMLWVPSSGDVVMQSPSLPVTLGQPASISCRSSQSLVYSDGNTHLNW 60

Qy      61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
          |||||:|||| || |||||:|||||:||||:||||:| |||:|
Db      61 FQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGTDFTLKISRVEAEDVGVYYCMQGTHWP 120

Qy      121 RTFGGGTKLEIK 132
          ||| |||||
Db      121 YTFGQGTKLEIK 132
```

RESULT 11

S22902

Ig kappa chain V region - human

C;Species: Homo sapiens (man)

C;Date: 19-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000

C;Accession: S22902

R;Chastagner, P.; Theze, J.; Zouali, M.

Gene 101, 305-306, 1991

A;Title: Cloning of a gene encoding a lupus-associated human autoantibody V(K) region using the polymerase chain reaction and degenerate primers.

A;Reference number: S22902; MUID:91276289; PMID:1905262

A;Accession: S22902

A;Status: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-142 <CHA>

A;Cross-references: EMBL:X56510

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;47-126/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 513; DB 2; Length 142;  
Best Local Similarity 74.0%; Pred. No. 2.7e-37;  
Matches 97; Conservative 16; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNQYVVMQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNW 60  
| ||| | ||:| |::| ||||:|:| | |:|||||:||||: ||| ||||  
Db 12 MRLPAQLLGLLMLWVPGSSGDVVMQTSPLSLPVTLGQPASISCRSSQSLVHSDGNTYLNW 71

Qy 61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIFAEDLGLYYCWQGTHTFP 120  
|||||:|||| | | ||||||:|||||:|||||:|:| | |||:|  
Db 72 FQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDVGYYCMQGTHTWP 131

Qy 121 RTFGGGTKLEI 131  
||| ||:| |  
Db 132 FTFGQGTREI 142

RESULT 12

S40324

Ig kappa chain V region - human

C;Species: Homo sapiens (man)

C;Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 09-Jul-2004

C;Accession: S40324

R;Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A;Title: Expressed human immunoglobulin chi genes and their hypermutation.

A;Reference number: S40312; MUID:94080891; PMID:8258341

A;Accession: S40324

A;Status: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-133 <KLE>

A;Cross-references: UNIPROT:Q8TCD0; EMBL:X72434

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;33-112/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 512; DB 2; Length 133;  
 Best Local Similarity 74.4%; Pred. No. 3.1e-37;  
 Matches 96; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

```

Qy      4 PAQFLFLLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNWLLQ 63
      ||| | ||:|:  ::| ||:|:|:| ||:| |||||:| |||: ||||| |
Db      1 PAQLLGLLMLWVPGSSGDVVLTSPLSLPVTLGQPASISCRSDQSLVYSDGKTYLNWYQQ 60

Qy     64 RPGQSPKRLLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTF 123
      |||||:|||| || ||||| |||||:|:|:|:|:| |||:| |||:| ||
Db     61 RPGQSPRRLLIYKVSNRDSGVPDRFTGSGSGTDFTLKISRVEAEDVGYYCMQGTHWPGTF 120

Qy    124 GGGTKLEIK 132
      | |||:|
Db    121 GQGTKVEIK 129
  
```

# RESULT 13

K2HURP

Ig kappa chain precursor V-II region (RPMI) - human

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 09-Jul-2004

C;Accession: A01890

R;Klobeck, H.G.; Meindl, A.; Combriato, G.; Solomon, A.; Zachau, H.G.

Nucleic Acids Res. 13, 6499-6513, 1985

A;Title: Human immunoglobulin kappa light chain genes of subgroups II and III.

A;Reference number: A93588; MUID:86041852; PMID:2997711

A;Accession: A01890

A;Molecule type: DNA

A;Residues: 1-133 <KLO>

A;Cross-references: UNIPROT:P06310

A;Note: the sequence was determined from the differentiated gene

C;Genetics:

A;Gene: GDB:IGKV2

A;Cross-references: GDB:136265

A;Map position: 2p12-2p12

A;Introns: 17/1

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-133/Product: Ig kappa chain V-II region (RPMI) #status predicted <MAT>

F;21-43/Region: framework 1

F;36-115/Domain: immunoglobulin homology <IMM>

F;44-59/Region: complementarity-determining 1

F;60-74/Region: framework 2

F;75-81/Region: complementarity-determining 2

F;82-113/Region: framework 3

F;114-122/Region: complementarity-determining 3

F;123-133/Region: framework 4

F;43-113/Disulfide bonds: #status predicted

Query Match 73.4%; Score 508; DB 1; Length 133;  
 Best Local Similarity 73.5%; Pred. No. 6.9e-37;

Matches 97; Conservative 16; Mismatches 19; Indels 0; Gaps 0;

```
Qy      1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLLDSGKTYLNW 60
          |  ||| | ||:|:  ::| ||||:|:| | |:|||||:||||: ||| ||||
Db      1 MRLPAQLLGLLMLWVPGSSGDVVMTQSPLSLPVTLGQPASISCRSSQSLVSDGNTYLNW 60

Qy     61 LLQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
          |||||:|||| ||  |||:||||:|||||:|||||:||||:|:| ||| |||:
Db     61 FQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWS 120

Qy     121 RTFGGGTKLEIK 132
          ||| ||:|
Db     121 WTFGQGTKVEIK 132
```

RESULT 14

S22658

Ig kappa chain precursor V region (0-81VL) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 29-Jan-1998 #sequence\_revision 06-Feb-1998 #text\_change 09-Jul-2004

C;Accession: S22658

R;Hirabayashi, Y.; Munakata, Y.; Sasaki, T.; Sano, H.

Nucleic Acids Res. 20, 2601, 1992

A;Title: Variable regions of a human anti-DNA antibody O-81 possessing lupus nephritis-associated idiootype.

A;Reference number: S22657; MUID:92285150; PMID:1598223

A;Accession: S22658

A;Molecule type: mRNA

A;Residues: 1-140 <HIR>

A;Cross-references: UNIPROT:Q8TCD0; EMBL:X59135

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-19/Domain: signal sequence #status predicted.<SIG>

F;20-140/Product: Ig kappa chain (fragment) #status predicted <MAT>

F;36-115/Domain: immunoglobulin homology <IMM>

Query Match 72.6%; Score 502.5; DB 2; Length 140;

Best Local Similarity 73.7%; Pred. No. 2.2e-36;

Matches 98; Conservative 15; Mismatches 19; Indels 1; Gaps 1;

```
Qy      1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLLDSGKTYLNW 60
          |  ||| | ||:|:  ::| ||||:|:| | |:|||||:||||: ||| ||||
Db      1 MRLPAQLLGLLMLWVPGSSGDVVMTQSPLSLPVTLGQPASISCRSSQSLVHSDGNTYLNW 60

Qy     61 LLQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHF- 119
          |||||:|||| ||  |||:||||:|||||:|||||:||||:|:| ||| | |:
Db     61 FQQRPGQSPRRLIYRVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQHTHWS 120

Qy     120 PRTEGGGKLEIK 132
          | ||| ||:|
Db     121 PITFGQGRLEIK 133
```

RESULT 15

A24452

Ig kappa chain precursor V-II region (RPMI 6410) - human

C;Species: Homo sapiens (man)

C;Date: 24-Jan-1988 #sequence\_revision 09-Aug-1996 #text\_change 16-Jul-1999  
 C;Accession: A24452  
 R;Weir, L.; Leder, P.  
 Nucleic Acids Res. 14, 3957-3970, 1986  
 A;Title: Structure and expression of a human subgroup II immunoglobulin kappa gene.  
 A;Reference number: A24452; MUID:86232631; PMID:3086847  
 A;Accession: A24452  
 A;Molecule type: DNA  
 A;Residues: 1-133 <WEI>  
 A;Cross-references: GB:M36859; NID:g185932; PIDN:AAA58920.1; PID:g185933  
 A;Note: this sequence was determined from the differentiated gene  
 C;Genetics:  
 A;Gene: GDB:IGKV2  
 A;Cross-references: GDB:136265  
 A;Map position: 2p12-2p12  
 A;Introns: 17/1  
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;1-20/Domain: signal sequence #status predicted <SIG>  
 F;21-133/Product: Ig kappa chain V-II region (RPMI 6410) #status predicted <MAT>  
 F;36-115/Domain: immunoglobulin homology <IMM>  
 F;43-113/Disulfide bonds: #status predicted

Query Match 71.7%; Score 496; DB 1; Length 133;  
 Best Local Similarity 72.7%; Pred. No. 7.4e-36;  
 Matches 96; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

Qy	1	MMSPAQFLFLLVLWIRETNGYVVM	QTPLT	LSVTIGQPASISCKSSQSL	LDSDGKTYLNW	60
		:	::       :	:     :	:	
Db	1	MRLPAQLLGLLRLWVP	GSSGDVVM	TQSP	LSLPVTLGQPASISCRSSQSLV	SDRNTYLNW 60
Qy	61	LLQRPQGSPKRLIYLVSKLDSGVP	DRFTGSGSGTDF	TLKISR	IEAEDLGLYYCWQGT	HFP 120
		:	:	:	: :	:
Db	61	FQQRPGQSPRRLIYKVS	NRDSGVPDR	FSGSGSGTDF	TLKISRVEAEDVG	VYYCMQGT
						HWS 120
Qy	121	RTFGGGTKLEIK				132
		:				
Db	121	WTFGQGTKVEIK				132

Search completed: December 13, 2004, 19:18:39  
 Job time : 25.4667 secs

OM protein - protein search, using sw model

Run on: December 13, 2004, 19:17:53 ; Search time 94.8444 Seconds  
(without alignments)  
497.104 Million cell updates/sec

Title: US-10-010-942B-2  
Perfect score: 692  
Sequence: 1 MMSPAQFLFLLVLWIRETNG.....CWQGTHFPRTFGGGTKLEIK 132

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	692	100.0	132	14	US-10-010-942B-2	Sequence 2, Appli
2	692	100.0	132	15	US-10-388-389-2	Sequence 2, Appli
3	692	100.0	132	16	US-10-703-713-2	Sequence 2, Appli
4	692	100.0	132	16	US-10-704-070-2	Sequence 2, Appli
5	650	93.9	135	9	US-09-881-823-10	Sequence 10, Appl
6	649	93.8	131	15	US-10-462-062-163	Sequence 163, App
7	646	93.4	131	15	US-10-462-062-164	Sequence 164, App
8	640	92.5	132	14	US-10-010-942B-5	Sequence 5, Appli
9	640	92.5	132	15	US-10-388-389-5	Sequence 5, Appli
10	640	92.5	132	16	US-10-703-713-5	Sequence 5, Appli
11	640	92.5	132	16	US-10-704-070-5	Sequence 5, Appli
12	636	91.9	132	13	US-10-006-773-11	Sequence 11, Appl
13	630	91.0	132	14	US-10-010-942B-11	Sequence 11, Appl
14	630	91.0	132	15	US-10-388-389-11	Sequence 11, Appl
15	630	91.0	132	16	US-10-703-713-11	Sequence 11, Appl
16	630	91.0	132	16	US-10-704-070-11	Sequence 11, Appl
17	606	87.6	142	9	US-09-840-459-102	Sequence 102, App
18	606	87.6	142	16	US-10-766-773-102	Sequence 102, App
19	606	87.6	142	16	US-10-766-610-102	Sequence 102, App
20	606	87.6	142	16	US-10-733-563-102	Sequence 102, App
21	562	81.2	353	10	US-09-203-958A-4	Sequence 4, Appli
22	560	80.9	112	9	US-09-835-087-1	Sequence 1, Appli
23	560	80.9	112	9	US-09-809-739-11	Sequence 11, Appl
24	560	80.9	112	9	US-09-840-459-9	Sequence 9, Appli
25	560	80.9	112	16	US-10-766-773-9	Sequence 9, Appli
26	560	80.9	112	16	US-10-766-610-9	Sequence 9, Appli
27	560	80.9	112	16	US-10-733-563-9	Sequence 9, Appli
28	560	80.9	122	15	US-10-272-899A-86	Sequence 86, Appl
29	560	80.9	130	15	US-10-272-899A-88	Sequence 88, Appl
30	559	80.8	112	15	US-10-462-062-149	Sequence 149, App
31	559	80.8	112	15	US-10-462-062-150	Sequence 150, App
32	556	80.3	112	9	US-09-840-459-54	Sequence 54, Appl
33	556	80.3	112	16	US-10-766-773-54	Sequence 54, Appl
34	556	80.3	112	16	US-10-766-610-54	Sequence 54, Appl
35	556	80.3	112	16	US-10-733-563-54	Sequence 54, Appl
36	551	79.6	500	14	US-10-168-809-22	Sequence 22, Appl
37	548	79.2	112	9	US-09-772-120-6	Sequence 6, Appli
38	548	79.2	535	9	US-09-968-851-38	Sequence 38, Appl
39	547	79.0	162	14	US-10-410-907A-30	Sequence 30, Appl
40	546	78.9	112	14	US-10-323-903-1	Sequence 1, Appli
41	538	77.7	112	9	US-09-835-087-5	Sequence 5, Appli
42	538	77.7	112	9	US-09-809-739-16	Sequence 16, Appl
43	538	77.7	112	9	US-09-840-459-14	Sequence 14, Appl
44	538	77.7	112	16	US-10-766-773-14	Sequence 14, Appl
45	538	77.7	112	16	US-10-766-610-14	Sequence 14, Appl

#### ALIGNMENTS

RESULT 1

US-10-010-942B-2

; Sequence 2, Application US/10010942B

; Publication No. US20030165496A1



```
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002
; CURRENT APPLICATION NUMBER: US/10/010,942B
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-10-010-942B-2
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```
Query Match          100.0%; Score 692; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 5.4e-57;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 MMSPAQFLFLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNW 60
|||||
Db      1 MMSPAQFLFLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNW 60

Qy     61 LLQRPQGSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGT HFP 120
|||||
Db     61 LLQRPQGSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGT HFP 120

Qy    121 RTFGGGTKLEIK 132
|||||
Db    121 RTFGGGTKLEIK 132
```

# RESULT 2

US-10-388-389-2

```
; Sequence 2, Application US/10388389
; Publication No. US2004008777A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/388,389
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
```

; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 132  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: (1)...(20)  
US-10-388-389-2

Query Match 100.0%; Score 692; DB 15; Length 132;  
Best Local Similarity 100.0%; Pred. No. 5.4e-57;  
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMQTPTLTLSTIGQPASISCKSSQSLDSDGKTYLNW 60  
|||||  
Db 1 MMSPAQFLFLLVLWIRETNGYVVMQTPTLTLSTIGQPASISCKSSQSLDSDGKTYLNW 60  
  
Qy 61 LLQRPQGSPKRLIYLVSKLD SGVPDRFTGSGSGTDFTLKISR IEAEDLGLYYCWQGT HFP 120  
|||||  
Db 61 LLQRPQGSPKRLIYLVSKLD SGVPDRFTGSGSGTDFTLKISR IEAEDLGLYYCWQGT HFP 120  
  
Qy 121 RTFGGGTKLEIK 132  
|||||  
Db 121 RTFGGGTKLEIK 132

RESULT 3

US-10-703-713-2

; Sequence 2, Application US/10703713  
; Publication No. US20040171815A1  
; GENERAL INFORMATION:  
; APPLICANT: Basi, Guriq  
; APPLICANT: Saldanha, Jose  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE  
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE  
; FILE REFERENCE: ELN-002CP  
; CURRENT APPLICATION NUMBER: US/10/703,713  
; CURRENT FILING DATE: 2003-11-07  
; PRIOR APPLICATION NUMBER: US/10/388,389  
; PRIOR FILING DATE: 2003-03-12  
; PRIOR APPLICATION NUMBER: US 10/010,942  
; PRIOR FILING DATE: 2001-12-06  
; PRIOR APPLICATION NUMBER: US 60/251,892  
; PRIOR FILING DATE: 2000-12-06  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 132  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: (1)...(20)  
US-10-703-713-2

Query Match 100.0%; Score 692; DB 16; Length 132;  
Best Local Similarity 100.0%; Pred. No. 5.4e-57;  
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLDSDGKTYLNW 60
        |||
Db      1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLDSDGKTYLNW 60

Qy     61 LLQRPQGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTTHFP 120
        |||
Db     61 LLQRPQGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTTHFP 120

Qy    121 RTFGGGTKLEIK 132
        |||
Db    121 RTFGGGTKLEIK 132
```

RESULT 4

US-10-704-070-2

; Sequence 2, Application US/10704070  
; Publication No. US20040171816A1  
; GENERAL INFORMATION:  
; APPLICANT: Basi, Guriq  
; APPLICANT: Saldanha, Jose  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE  
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE  
; FILE REFERENCE: ELN-002CP  
; CURRENT APPLICATION NUMBER: US/10/704,070  
; CURRENT FILING DATE: 2003-11-07  
; PRIOR APPLICATION NUMBER: 10/388,389  
; PRIOR FILING DATE: 2003-03-12  
; PRIOR APPLICATION NUMBER: US 10/010,942  
; PRIOR FILING DATE: 2001-12-06  
; PRIOR APPLICATION NUMBER: US 60/251,892  
; PRIOR FILING DATE: 2000-12-06  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 132  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: (1)...(20)

US-10-704-070-2

Query Match 100.0%; Score 692; DB 16; Length 132;  
Best Local Similarity 100.0%; Pred. No. 5.4e-57;  
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLDSDGKTYLNW 60
        |||
Db      1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLDSDGKTYLNW 60

Qy     61 LLQRPQGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTTHFP 120
        |||
```

Db 61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTTHFP 120

Qy 121 RTFGGGTKLEIK 132  
 |||||

Db 121 RTFGGGTKLEIK 132

RESULT 5

US-09-881-823-10

; Sequence 10, Application US/09881823  
 ; Patent No. US20020068066A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SHI, WENYUAN  
 ; APPLICANT: ANDERSON, MAXWELL  
 ; APPLICANT: MORRISON, SHERIE  
 ; APPLICANT: TRINH, RYAN  
 ; APPLICANT: WIMS, LETITIA  
 ; APPLICANT: CHEN, LI  
 ; TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries  
 ; FILE REFERENCE: 22851-032  
 ; CURRENT APPLICATION NUMBER: US/09/881,823  
 ; CURRENT FILING DATE: 2001-06-15  
 ; PRIOR APPLICATION NUMBER: US 07/378,577  
 ; PRIOR FILING DATE: 1999-08-20  
 ; NUMBER OF SEQ ID NOS: 32  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 10  
 ; LENGTH: 135  
 ; TYPE: PRT  
 ; ORGANISM: Murine  
 US-09-881-823-10

Query Match 93.9%; Score 650; DB 9; Length 135;  
 Best Local Similarity 93.2%; Pred. No. 4.7e-53;  
 Matches 123; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVMTQTPLTSLVTIGQPASISCKSSQSLLDSGKTYLW 60  
 |||||

Db 1 MMSPAQFLFLLVLWIRETNGDVMTQTPLTSLVTIGQPASISCKSSQSLLDRDGRYLSW 60

Qy 61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTTHFP 120  
 |||||

Db 61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTTHFP 120

Qy 121 RTFGGGTKLEIK 132  
 ||| |||||

Db 121 LTFGAGTKLELK 132

RESULT 6

US-10-462-062-163

; Sequence 163, Application US/10462062  
 ; Publication No. US20040044187A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SATO, KOH  
 ; APPLICANT: ADACHI, HIDEKI  
 ; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)

```
; TITLE OF INVENTION:  AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
; FILE REFERENCE: 053466-0360
; CURRENT APPLICATION NUMBER: US/10/462,062
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 163
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Full-length amino
acid
; OTHER INFORMATION: sequence for L chain V region of anti-TF mouse monoclonal
; OTHER INFORMATION: antibody ATR-7
US-10-462-062-163
```

```
Query Match          93.8%;  Score 649;  DB 15;  Length 131;
Best Local Similarity 93.9%;  Pred. No. 5.7e-53;
Matches 123;  Conservative 4;  Mismatches 4;  Indels 0;  Gaps 0;
```

```
Qy      2 MSPAQFLFLLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLLDSGKTYLNWL 61
        |||||
Db      1 MSPAQFLFLLVLWIREINGDVVLTQTPLTSLVTIGQPASVSCCKSSQSLLDSGKTYLNWL 60
        |||||

Qy      62 LQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPR 121
        |||||
Db      61 LQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQDTHFPD 120
        |||||

Qy      122 TFGGGTKLEIK 132
        |||||
Db      121 TFGGGTKLEIK 131
```

# RESULT 7

```
US-10-462-062-164
; Sequence 164, Application US/10462062
; Publication No. US20040044187A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
; TITLE OF INVENTION:  AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
; FILE REFERENCE: 053466-0360
; CURRENT APPLICATION NUMBER: US/10/462,062.
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 164
```

```
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Full-length amino
acid
; OTHER INFORMATION: sequence for L chain V region of anti-TF mouse monoclonal
; OTHER INFORMATION: antibody ATR-8
US-10-462-062-164
```

```
Query Match          93.4%;  Score 646;  DB 15;  Length 131;
Best Local Similarity 93.1%;  Pred. No. 1.1e-52;
Matches 122;  Conservative 5;  Mismatches 4;  Indels 0;  Gaps 0;
```

```
Qy      2 MSPAQFLFLLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWL 61
          |||||: || ||:|||||:|||||:|||||:|||||
Db      1 MSPAQFLFLLVLWIRDINGDVVLTQTPLTSLVTIGQPASVSCKSSQSLDSDGKTYLNWL 60

Qy      62 LQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGFHPR 121
          |||||:|||||:|||||:|||||
Db      61 LQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGYYCWQDTHFPD 120

Qy      122 TFGGGTKLEIK 132
          |||||
Db      121 TFGGGTKLEIK 131
```

#### RESULT 8

```
US-10-010-942B-5
; Sequence 5, Application US/10010942B
; Publication No. US20030165496A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002
; CURRENT APPLICATION NUMBER: US/10/010,942B
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
; OTHER INFORMATION: humanized 3D6 light chain variable region
US-10-010-942B-5
```

```
Query Match          92.5%;  Score 640;  DB 14;  Length 132;
Best Local Similarity 90.2%;  Pred. No. 4e-52;
Matches 119;  Conservative 10;  Mismatches 3;  Indels 0;  Gaps 0;
```

Qy	1	MMSPAQFLFLLVLWIRETNGYVVM	QTPLTSLSVTIGQPASISCKSSQSL	LLSDSGKTYLNW	60
Db	1	MMSPAQFLFLLVLWIRETNGYVVM	QSPLSLPVTGPGEPAISCKSSQSL	LLSDSGKTYLNW	60
Qy	61	LLQRPQGSPKRLIYLVSKLDSGVP	DRFTGSGSGTDFTLKISR	IEAEDLGLYYCWQGT	120
		:			
Db	61	LLQKPGQSPQRLIYLVSKLDSGVP	DRFSGSGSGTDFTLKISR	VEAEDVG	120
		:			
Qy	121	RTFGGGTKLEIK	132		
			:		
Db	121	RTFGQGTKVEIK	132		

US-10-388-389-5

```
; Sequence 5, Application US/10388389
; Publication No. US20040087777A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/388,389
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 132
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: (1)...(20)
;   OTHER INFORMATION: humanized 3D6 light chain variable region
US-10-388-389-5
```

```

Qy      1 MMSPAQFLFLLVLWIRETNGYVVMQTPTLTSVTIGQPASISCKSSQSLDSDGKTYLNW 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MMSPAQFLFLLVLWIRETNGYVVMQTSPLSLPVTPGEPASISCKSSQSLDSDGKTYLNW 60

Qy     61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGT HFP 120
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     61 LLQKPGQSPQRLLIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVIYCWQGT HFP 120

Qy    121 RTFGGGTKLEIK 132
        ||| |||: |||

```

## RESULT 10

US-10-703-713-5

```
; Sequence 5, Application US/10703713
; Publication No. US20040171815A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/703,713
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
; OTHER INFORMATION: humanized 3D6 light chain variable region
US-10-703-713-5
```

Query Match 92.5%; Score 640; DB 16; Length 132;  
Best Local Similarity 90.2%; Pred. No. 4e-52;  
Matches 119; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

Qy	1	MMSPAQFLFLLVLWIRETNGYVVM	QTPLT	LSVTIGQPASIS	CKSSQSL	LDSDGKTYL	NW	60
Db	1	MMSPAQFLFLLVLWIRETNGYVVM	QSPLSLP	VTGPGE	PASIS	CKSSQSL	LDSDGKTYL	NW 60
Qy	61	LLQRPQGSPKRLIYLVSKLDSG	VPDRFTG	SGSGTDF	TLKISR	IEAEDLGL	YYCWQG	THFP 120
		:						
Db	61	LLQKPGQSPQR	LIYLVSKLDSG	VPDRFSG	SGSGTDF	TLKISR	VEAEDVG	VYYCWQGTHFP 120
		:						
Qy	121	RTFGGGTKLEIK	132					
			:					
Db	121	RTFGGQTKVEIK	132					

## RESULT 11

US-10-704-070-5

```
; Sequence 5, Application US/10704070
; Publication No. US20040171816A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurig
```



```
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/704,070
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: 10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
; OTHER INFORMATION: humanized 3D6 light chain variable region
US-10-704-070-5
```

```
Query Match          92.5%; Score 640; DB 16; Length 132;
Best Local Similarity 90.2%; Pred. No. 4e-52;
Matches 119; Conservative 10; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLLDSGKTYLNW 60
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 MMSPAQFLFLLVLWIRETNGYVVMQTSPLSLPVTPGEPASISCKSSQSLLDSGKTYLNW 60

Qy     61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     61 LLQKPGQSPQRLIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFP 120

Qy     121 RTFGGGTKLEIK 132
          |||| |||:|||
Db     121 RTFGQGTKVEIK 132
```

```
RESULT 12
US-10-006-773-11
; Sequence 11, Application US/10006773
; Publication No. US20020132983A1
; GENERAL INFORMATION:
; APPLICANT: Junghans, Richard P.
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against
Tumor Antigens
; FILE REFERENCE: 003
; CURRENT APPLICATION NUMBER: US/10/006,773
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/250,089
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
```



```

Qy      61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 LLQKPGQSPQRLIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFP 120

Qy      121 RTFGGGTKLEIK 132
      |||| |||:|||
Db      121 RTFGQGTKVEIK 132

```

RESULT 14

US-10-388-389-11

```

; Sequence 11, Application US/10388389
; Publication No. US2004008777A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/388,389
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
; OTHER INFORMATION: humanized 3D6 light chain variable region
US-10-388-389-11

```

```

Query Match          91.0%;  Score 630;  DB 15;  Length 132;
Best Local Similarity 89.4%;  Pred. No. 3.4e-51;
Matches 118;  Conservative 10;  Mismatches 4;  Indels 0;  Gaps 0;

```

```

Qy      1 MMSPAQFLFLLVLWIRETNGYVVMQTPTLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 MMSPAQFLFLLVLWIRETNGDVVMQTQSPLSLPVTPGEPASISCKSSQSLLSDGKTYLNW 60

Qy      61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 LLQKPGQSPQRLIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFP 120

Qy      121 RTFGGGTKLEIK 132
      |||| |||:|||
Db      121 RTFGQGTKVEIK 132

```

RESULT 15



OM protein - protein search, using sw model

Run on: December 13, 2004, 18:50:06 ; Search time 125.644 Seconds  
 (without alignments)  
 604.479 Million cell updates/sec

Title: US-10-010-942B-2  
 Perfect score: 692  
 Sequence: 1 MMSPAQFLFLVLWIRETNG.....CWQGLTFPRTFGGGTKLEIK 132

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : UniProt\_02:\*  
 1: uniprot\_sprot:\*  
 2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	611	88.3	148	2	Q8K122	Q8k122 mus musculu
2	583	84.2	239	2	Q8K0F8	Q8k0f8 mus musculu
3	511	73.8	239	2	Q8TCD0	Q8tcd0 homo sapien
4	508	73.4	133	1	KV2F_HUMAN	P06310 homo sapien
5	471	68.1	239	2	Q6P491	Q6p491 homo sapien
6	471	68.1	239	2	Q8NEK0	Q8nek0 homo sapien
7	471	68.1	239	2	AAH63599	Aah63599 homo sapi
8	460	66.5	238	2	Q99M37	Q99m37 mus musculu
9	459	66.3	238	2	Q8VCI6	Q8vci6 mus musculu
10	453	65.5	239	2	Q8VC55	Q8vc55 mus musculu
11	448	64.7	239	2	BAC04905	Bac04905 homo sapi
12	444.5	64.2	114	2	Q9UL80	Q9ul80 homo sapien
13	441.5	63.8	240	2	Q6PIH6	Q6pih6 homo sapien
14	441.5	63.8	240	2	AAH34142	Aah34142 homo sapi
15	436	63.0	114	2	AAR11017	Aar11017 mus muscu

16	434	62.7	113	1	KV2G_MOUSE	P01631 mus musculu
17	417	60.3	117	1	KV2E_HUMAN	P06309 homo sapien
18	415	60.0	113	1	KV2D_HUMAN	P01617 homo sapien
19	414.5	59.9	115	1	KV2A_HUMAN	P01614 homo sapien
20	414	59.8	113	1	KV2B_HUMAN	P01615 homo sapien
21	411	59.4	105	2	AAR11074	Aar11074 mus muscu
22	408.5	59.0	104	2	AAR11056	Aar11056 mus muscu
23	406	58.7	104	2	AAR11064	Aar11064 mus muscu
24	405	58.5	104	2	AAR11024	Aar11024 mus muscu
25	398	57.5	104	2	Q9JL82	Q9jl82 mus musculu
26	398	57.5	109	2	AAR10990	Aar10990 mus muscu
27	397	57.4	104	2	AAR11063	Aar11063 mus muscu
28	394	56.9	102	2	AAR11040	Aar11040 mus muscu
29	389.5	56.3	112	1	KV2C_HUMAN	P01616 homo sapien
30	388	56.1	113	1	KV2F_MOUSE	P01630 mus musculu
31	386	55.8	129	1	KV3L_HUMAN	P18135 homo sapien
32	381	55.1	112	2	Q6LEM8	Q6lem8 mus musculu
33	381	55.1	112	2	BAD00151	Bad00151 mus muscu
34	380.5	55.0	134	1	KV4C_HUMAN	P06314 homo sapien
35	380	54.9	113	1	KV2E_MOUSE	P03976 mus musculu
36	377.5	54.6	236	2	Q6PIL8	Q6pil8 homo sapien
37	377.5	54.6	236	2	AAH32451	Aah32451 homo sapi
38	376	54.3	235	2	Q6GMV9	Q6gmv9 homo sapien
39	374	54.0	112	1	KV2D_MOUSE	P01629 mus musculu
40	374	54.0	120	1	KV2B_MOUSE	P01627 mus musculu
41	373.5	54.0	131	1	KV3I_MOUSE	P01661 mus musculu
42	373	53.9	113	1	KV2C_MOUSE	P01628 mus musculu
43	373	53.9	129	1	KV3M_HUMAN	P18136 homo sapien
44	373	53.9	133	1	KV4B_HUMAN	P06313 homo sapien
45	369.5	53.4	240	2	Q6PJB5	Q6pjb5 homo sapien

# ALIGNMENTS

## RESULT 1

Q8K122

ID Q8K122 PRELIMINARY; PRT; 148 AA.  
AC Q8K122;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FVB/N; TISSUE=Salivary gland;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Salivary gland;  
 RA Strausberg R.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC028925; AAH28925.1; -.  
 DR HSSP; Q8K0F8; 1KN2.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; ig; 1.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 148 AA; 16345 MW; 183920BBD9F3B521 CRC64;

Query Match 88.3%; Score 611; DB 2; Length 148;  
 Best Local Similarity 97.5%; Pred. No. 3.8e-51;  
 Matches 116; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 MSPAQFLFLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWL 61  
 ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||  
 Db 1 MSPAQFLFLLVLWIRETNGDVVMQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWL 60  
 QY 62 LQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGT HFP 120  
 |||||||||||||||||||||||||||||||||||||:|||||:|||||||  
 Db 61 LQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGT HFP 119

# RESULT 2

Q8K0F8

ID Q8K0F8 PRELIMINARY; PRT; 239 AA.  
 AC Q8K0F8; ----  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=mix FVB/N;





Qy 61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGT HFP 120  
 Db 61 LLQRPQGSPKRLISLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCLQST HFP 120

Qy 121 RTFGGGTKLEIK 132  
 Db 121 YTFGGGTKLEIK 132

# RESULT 3

Q8TCD0

ID Q8TCD0 PRELIMINARY; PRT; 239 AA.  
 AC Q8TCD0;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RA Strausberg R.;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC022362; AAH22362.1; -.  
 DR PIR; S22658; S22658.  
 DR PIR; S34095; S34095.  
 DR PIR; S40324; S40324.  
 DR PIR; S40374; S40374.  
 DR PIR; S42267; S42267.  
 DR PIR; S42268; S42268.

DR HSSP; P01834; 1I7Z.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; C1-set; 1.  
 DR Pfam; PF00047; ig; 1.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 239 AA; 26234 MW; FAGEDC3A3B03871D CRC64;

Query Match 73.8%; Score 511; DB 2; Length 239;  
 Best Local Similarity 72.7%; Pred. No. 3.2e-41;  
 Matches 96; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLVLWIRETNGYVVMQTPTLTLVTIGQPASISCKSSQSLDSDGKTYLNW 60  
 | ||| | ||:|: ::| ||||:|:| | |:|||||:|:|:| ||| |||||  
 Db 1 MRLPAQLLGLLMLWVPGSSGDVVMQTSPSLPVTLGQPASISCRSTQSLVYSDGNTYLNW 60  
 Qy 61 LLQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTTHFP 120  
 |||||:| ||| || |||||:| |||||:|:|:| |:|:|:| |||:|  
 Db 61 FQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKITRVEAEDVGVYFCMQGTHWP 120  
 Qy 121 RTFGGGTKLEIK 132  
 ||| |||||  
 Db 121 STFGQGTKLEIK 132

#### RESULT 4

##### KV2F\_HUMAN

ID KV2F\_HUMAN STANDARD; PRT; 133 AA.  
 AC P06310;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-II region RPMI 6410 precursor.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86041852; PubMed=2997711;  
 RA Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;  
 RT "Human immunoglobulin kappa light chain genes of subgroups II and  
 RT III.";  
 RL Nucleic Acids Res. 13:6499-6513(1985).

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

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CC -----
DR EMBL; Z00020; CAA77315.1; -.
DR PIR; A01890; K2HURP.
DR HSSP; Q99M37; 1I9I.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL          1      20
FT CHAIN           21     133      Ig kappa chain V-II region RPMI 6410.
FT DOMAIN          21      43      Framework-1.
FT DOMAIN          44      59      Complementarity-determining-1.
FT DOMAIN          60      74      Framework-2.
FT DOMAIN          75      81      Complementarity-determining-2.
FT DOMAIN          82     113      Framework-3.
FT DOMAIN         114     122      Complementarity-determining-3.
FT DOMAIN         123     132      Framework-4.
FT DISULFID        43     113      By similarity.
FT NON_TER        133     133
SQ SEQUENCE       133 AA;  14707 MW;  513CCAF3673009EE CRC64;

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Query Match          73.4%;  Score 508;  DB 1;  Length 133;
Best Local Similarity 73.5%;  Pred. No. 3.2e-41;
Matches   97;  Conservative   16;  Mismatches   19;  Indels      0;  Gaps      0;

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Qy      1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNW 60
      |  ||| | ||:|:  ::| |||||:|:| ||:|||||||:||||: ||| |||||
Db      1 MRLPAQLLGLLMLWVPGSSGDVVMQTSPSLPVTLGQPASISCRSSQSLVYSDGNTYLNW 60

Qy     61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
      |||||:|||| ||  |||||:|||||||:|||||:||||:|:| |||||
Db     61 FQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWS 120

Qy    121 RTFGGGTKLEIK 132
      ||| |||:|
Db    121 WTFGQGTKVEIK 132

```

# RESULT 5

Q6P491

```

ID   Q6P491          PRELIMINARY;      PRT;   239 AA.
AC   Q6P491;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.

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RC TISSUE=Skin;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skin;  
 RA Strausberg R.;  
 RL Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC063599; AAH63599.1; -.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; C1-set; 1.  
 DR Pfam; PF00047; ig; 2.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGc1; 1.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 239 AA; 26245 MW; CD7313DDFFD358B3 CRC64;

Query Match 68.1%; Score 471; DB 2; Length 239;

Best Local Similarity 68.8%; Pred. No. 2.4e-37;

Matches 88; Conservative 21; Mismatches 19; Indels 0; Gaps 0;

Qy 5 AQFLFLLVLWIRETNGYVVMQTPTLTLVSTIGQPASISCKSSQSLDSDGKTYLNWLLQR 64  
 || | ||:||: ::| :|||||: ||:|||||||: ||:||| |:| ||:| |  
 Db 5 AQLLGLLMLWVPGSSGDIVMTQTPLSSPVTLGQPASISCRSSESLHSNGNTYLSWLHQR 64  
 Qy 65 PGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGFHPRTEFG 124  
 ||| |: ||| :| |||||: ||: |||||: |||: |: ||| | : |||||  
 Db 65 PGQPPRLLIYKISNRFSGVDPDRFSGSGAGTDFTLKISRVEAEDVGVIYCMQVSHFPRTEFG 124  
 Qy 125 GGTKLEIK 132  
 ||: |||

## RESULT 6

## Q8NEK0

ID Q8NEK0 PRELIMINARY; PRT; 239 AA.  
AC Q8NEK0;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Prostate;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywiński M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Prostate;  
RA Strausberg R.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; BC030814; AAH30814.1; -.  
DR PIR; S23638; S23638.  
DR PIR; S34091; S34091.  
DR PIR; S40342; S40342.  
DR PIR; S40357; S40357.  
DR HSSP; P01834; 1I7Z.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; C1-set; 1.  
DR Pfam; PF00047; ig; 1.  
DR SMART; SM00406; IGv; 1.

DR PROSITE; PS50835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;

Query Match 68.1%; Score 471; DB 2; Length 239;  
Best Local Similarity 68.2%; Pred. No. 2.4e-37;  
Matches 90; Conservative 19; Mismatches 23; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNW 60  
| ||| | ||:|: ::| :|||:|:| | | :| |||||:| |||| | || | ||:|  
Db 1 MRLPAQLLGLLMLWVSGSSGDIVMTQSPLSLPVTPGEPASISCRSSQSLLDSDGYNYLDW 60  
  
Qy 61 LLQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTFFP 120  
||:|||||: |||| | |||||:|||||||:|||||:|:|||| | | |  
Db 61 YLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISKVEAEDVGIYYCMQGLQTP 120  
  
Qy 121 RTFGGGTKLEIK 132  
:||| |||:|||  
Db 121 QTFGQGTKVEIK 132

#### RESULT 7

AAH63599

ID AAH63599 PRELIMINARY; PRT; 239 AA.  
AC AAH63599;  
DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skin;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skin;  
 RA Strausberg R.;  
 RL Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC063599; AAH63599.1; -.  
 KW Hypothetical protein.  
 SQ SEQUENCE 239 AA; 26245 MW; CD7313DDFFD358B3 CRC64;

Query Match 68.1%; Score 471; DB 2; Length 239;  
 Best Local Similarity 68.8%; Pred. No. 2.4e-37;  
 Matches 88; Conservative 21; Mismatches 19; Indels 0; Gaps 0;

Qy 5 AQFLFLLVLWIRETNGYVVMQTPTLTLSTIGQPASISCKSSQSLDSDGKTYLNWLLQR 64  
 || | ||:||: ::| :|||||||: ||:|||||||: ||:||| | :| |||: || ||  
 Db 5 AQLLGLLMLWVPGSSGDIVMTQTPLSSPVTLGQPASISCRSSESLLHSNGNTYLSWLHQR 64  
 Qy 65 PGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHTFPRTFG 124  
 ||| | : ||| : | ||||| : ||| : ||||| ||||| : ||| : | : ||| | : ||||| ||  
 Db 65 PGQPPRLLIYKISNRFSGVPDRFSGSGAGTDFTLKISRVEAEDVGVIYCMQVSHFPRTFG 124  
 Qy 125 GGKLEIK 132  
 ||: |||  
 Db 125 QGTRVEIK 132

# RESULT 8

Q99M37

ID Q99M37 PRELIMINARY; PRT; 238 AA.  
 AC Q99M37;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=mix FVB/N;  
 RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=mix FVB/N;  
 RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;  
 RA Strausberg R.;  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC002035; AAH02035.1; -.  
 DR PIR; A31807; A31807.  
 DR PIR; A32248; A32248.  
 DR PIR; B32248; B32248.  
 DR PIR; C32248; C32248.  
 DR PIR; D28195; D28195.  
 DR PIR; E28195; E28195.  
 DR PIR; F27887; F27887.  
 DR PIR; F32530; F32530.  
 DR PIR; JL0029; JL0029.  
 DR PIR; PH1035; PH1035.  
 DR PIR; PH1036; PH1036.  
 DR PIR; PH1037; PH1037.  
 DR PIR; PH1038; PH1038.  
 DR PIR; PH1039; PH1039.  
 DR PIR; PH1040; PH1040.  
 DR PIR; PH1042; PH1042.  
 DR PIR; PH1043; PH1043.  
 DR PIR; PH1044; PH1044.  
 DR PIR; S07455; S07455.  
 DR PIR; S16112; S16112.  
 DR PIR; S24498; S24498.  
 DR PIR; S24500; S24500.  
 DR PIR; S24501; S24501.  
 DR PIR; S24502; S24502.  
 DR PIR; S24503; S24503.  
 DR PIR; S24504; S24504.  
 DR PIR; S24506; S24506.  
 DR PIR; S24507; S24507.  
 DR PIR; S24508; S24508.  
 DR PIR; S24509; S24509.  
 DR PIR; S24510; S24510.  
 DR PIR; S24529; S24529.  
 DR PIR; S24530; S24530.  
 DR PIR; S24531; S24531.  
 DR PIR; S24532; S24532.  
 DR PIR; S24533; S24533.  
 DR PIR; S24534; S24534.  
 DR PIR; S24535; S24535.  
 DR PIR; S24536; S24536.  
 DR PIR; S24537; S24537.  
 DR PIR; S24538; S24538.  
 DR PIR; S24539; S24539.  
 DR PDB; 1I9I; X-ray; L=20-238.



DR PDB; 1I9J; X-ray; L=20-238.  
 DR PDB; 1KTR; X-ray; L=17-132.  
 DR PDB; 1LO2; X-ray; L/X=20-238.  
 DR PDB; 1LO3; X-ray; L/X=20-238.  
 DR PDB; 1LO4; X-ray; L=20-236.  
 DR PDB; 2MPA; X-ray; L=20-238.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; C1-set; 1.  
 DR Pfam; PF00047; ig; 1.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match 66.5%; Score 460; DB 2; Length 238;  
 Best Local Similarity 69.6%; Pred. No. 2.7e-36;  
 Matches 87; Conservative 17; Mismatches 21; Indels 0; Gaps 0;

Qy 8 LFLVLWIRETNGYVVMQTPTLTLSTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQG 67  
 | : | | : : | | | | | : | | : | | | | : | | : | | | | | : | |  
 Db 7 LLVLMFWIPASSSDVVMQTPTLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQ 66  
 Qy 68 SPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGFHFPRTFGGGT 127  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 67 SPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVIYCFQGSHPVPTFGSGT 126  
 Qy 128 KLEIK 132  
 | | | |  
 Db 127 KLEIK 131

#### RESULT 9

##### Q8VCI6

ID Q8VCI6 PRELIMINARY; PRT; 238 AA.  
 AC Q8VCI6;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Colon;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Colon;  
 RA Strausberg R.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC019760; AAH19760.1; -.  
 DR PIR; A27887; A27887.  
 DR PIR; A32248; A32248.  
 DR PIR; A33933; A33933.  
 DR PIR; B27887; B27887.  
 DR PIR; B30577; B30577.  
 DR PIR; B31485; B31485.  
 DR PIR; B32248; B32248.  
 DR PIR; B41940; B41940.  
 DR PIR; C27887; C27887.  
 DR PIR; C32248; C32248.  
 DR PIR; C34904; C34904.  
 DR PIR; D27887; D27887.  
 DR PIR; D29380; D29380.  
 DR PIR; E28833; E28833.  
 DR PIR; E32530; E32530.  
 DR PIR; F32530; F32530.  
 DR PIR; H31485; H31485.  
 DR PIR; PH0106; PH0106.  
 DR PIR; PH1030; PH1030.  
 DR PIR; PH1031; PH1031.  
 DR PIR; PH1034; PH1034.  
 DR PIR; PH1045; PH1045.  
 DR PIR; PL0257; PL0257.  
 DR PIR; PT0178; PT0178.  
 DR PIR; PT0359; PT0359.  
 DR PIR; S07455; S07455.  
 DR PIR; S16112; S16112.  
 DR PIR; S26334; S26334.  
 DR PIR; S53750; S53750.  
 DR PIR; S60066; S60066.  
 DR PDB; 1A3R; X-ray; L=-.  
 DR PDB; 1ACY; X-ray; L=-.  
 DR PDB; 1H3P; X-ray; L=20-238.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF07654; Cl-set; 1.  
DR Pfam; PF00047; ig; 1.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;

Query Match 66.3%; Score 459; DB 2; Length 238;  
Best Local Similarity 70.4%; Pred. No. 3.4e-36;  
Matches 88; Conservative 16; Mismatches 21; Indels 0; Gaps 0;

Qy 8 LFLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPQG 67  
| :|: || :: |||||:| |::| ||||:||||: |:| |||:| ||:|  
Db 7 LLVLMFWIPASSSDVVMQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQ 66  
  
Qy 68 SPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHTFPRTFGGGT 127  
||| ||| || |||||:|||||:|||||:|||||:|:| | | | |||||  
Db 67 SPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPTFGGGT 126  
  
Qy 128 KLEIK 132  
|||||  
Db 127 KLEIK 131

RESULT 10

Q8VC55

ID Q8VC55 PRELIMINARY; PRT; 239 AA.  
AC Q8VC55;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FVB/N; TISSUE=Colon;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Colon;  
 RA Strausberg R.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC021781; AAH21781.1; -.  
 DR PIR; A33933; A33933.  
 DR PDB; 1KC5; X-ray; L=21-239.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; C1-set; 1.  
 DR Pfam; PF00047; ig; 1.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 239 AA; 26303 MW; C16119CACA25C337 CRC64;

Query Match 65.5%; Score 453; DB 2; Length 239;  
 Best Local Similarity 67.4%; Pred. No. 1.3e-35;  
 Matches 89; Conservative 16; Mismatches 27; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLSDGKTYLWN 60  
 | | : ||: :: ||:||||:| | || |||||::|||:|||||  
 Db 1 MKLPVLLVLLLLFTSPASSSDVLTQTPLSLPVNIGDQASISCKSTKSLNSDGFTYLDW 60  
  
 Qy 61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGYYCWQGTHTFP 120  
 ||:||||: ||||| |||||:|||||:|||||:|||||:||||:| |  
 Db 61 YLQKPGQSPQLLIYLVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGYYCFQSNHLP 120  
  
 Qy 121 RTFGGGTKLEIK 132  
 |||||  
 Db 121 YTFGGGTKLEIK 132

# RESULT 11

BAC04905

ID BAC04905 PRELIMINARY; PRT; 239 AA.  
 AC BAC04905;  
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
 DE CDNA FLJ39619 fis, clone SMINT2000984, highly similar to IG KAPPA  
 DE CHAIN V-II REGION GM607.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Small intestine;

RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,  
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,  
 RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,  
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,  
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,  
 RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,  
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,  
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,  
 RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,  
 RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,  
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,  
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,  
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,  
 RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,  
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,  
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,  
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,  
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,  
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,  
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,  
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,  
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,  
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,  
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,  
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,  
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,  
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;  
 RT "Complete sequencing and characterization of 21,243 full-length human  
 RT cDNAs.";  
 RL Nat. Genet. 36:40-45(2004).  
 DR EMBL; AK096938; BAC04905.1; -.  
 SQ SEQUENCE 239 AA; 25964 MW; 78D9005B0E5CA51E CRC64;

Query Match 64.7%; Score 448; DB 2; Length 239;  
 Best Local Similarity 64.4%; Pred. No. 4e-35;  
 Matches 85; Conservative 21; Mismatches 26; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLW 60  
 | ||| | ||:|: ::| :|||:|:| || |:|||||:||||| |:| |:|  
 Db 1 MRLPAQLLGLLMLWVSGSSGEIVMTQSPLSLPVTAGEPASISCRSSQSLHNGYNYVDW 60  
  
 Qy 61 LLQRPQGSPKRLIYLVSKLD SGVPDRFTGSGSGTDFTLKISR IEAEDLGLYYCWQGT HFP 120  
 ||:|||||: ||:| | |||||:||||||| |||||:|||||:|:|:| |  
 Db 61 YLQKPGQSPQLLIFLSSNRASGV PDRFSGSGSGTDFILKISRVEAEDVG VYFCMQALQMP 120  
  
 Qy 121 RTFGGGTKLEIK 132  
 ||| |||:|  
 Db 121 GTFGQGTKVEIK 132

# RESULT 12

Q9UL80

ID Q9UL80 PRELIMINARY; PRT; 114 AA.  
 AC Q9UL80;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Myosin-reactive immunoglobulin light chain variable region  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus.";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035034; AAD56270.1; -.  
 DR PIR; B49002; B49002.  
 DR PIR; S23638; S23638.  
 DR PIR; S34094; S34094.  
 DR PIR; S34095; S34095.  
 DR HSSP; Q99M37; 1I9I.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; ig; 1.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 114 114  
 SQ SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;

Query Match 64.2%; Score 444.5; DB 2; Length 114;  
 Best Local Similarity 76.8%; Pred. No. 3.8e-35;  
 Matches 86; Conservative 12; Mismatches 13; Indels 1; Gaps 1;

Qy 22 VVMTQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81  
 |||||:|:| ||: |||||:|||| : ||| |||| |||||:|||| || ||  
 Db 2 VVMTQSPLSLPVTLRQPASISCRSSQSPVYSDGNTYLNWFQQRPQGSPRRLIYKVSNRDS 61  
 Qy 82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPR-TFGGGTKLEIK 132  
 |||||:|||||:|||||:||||:| ||| |||:||||  
 Db 62 GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWPPWTFGQGTKVEIK 113

# RESULT 13

Q6PIH6

ID Q6PIH6 PRELIMINARY; PRT; 240 AA.  
 AC Q6PIH6;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE IGKV1-5 protein.  
 GN Name=IGKV1-5;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H.; Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RA Strausberg R.;  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC034142; AAH34142.1; -.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; C1-set; 1.  
 DR Pfam; PF00047; ig; 2.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGc1; 1.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 SQ SEQUENCE 240 AA; 26234 MW; 188D4DD8BB781EC4 CRC64;

Query Match 63.8%; Score 441.5; DB 2; Length 240;  
 Best Local Similarity 66.2%; Pred. No. 1.7e-34;  
 Matches 88; Conservative 17; Mismatches 27; Indels 1; Gaps 1;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMQTPTLTLSTIGQPASISCKSSQSLDSDGKTYLNW 60  
 | ||| | ||:||: :|| :|| |:||:|||| |:|||||:||||| |:| | :|  
 Db 1 MRLPAQLLGLLMLWVSGSSGDIVMAQSPLSLSVTPGEPASISCRSSQSLHNGYNYFDW 60  
  
 Qy 61 LLQRPGQSPKRLIYLVS KLDSGVPDRFTGSGSGTDFTLKISR IEAEDLGLYYCWQGTHF- 119  
 ||:|||||: ||| | ||||||:|||||||||||:||||:|:|||| |  
 Db 61 YLQKPGQSPQLLIYWG SNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP 120  
  
 Qy 120 PRTEGGG TKLEIK 132  
 | ||| |||||

Db 121 PYTFGQGTKLEIK 133

RESULT 14

AAH34142

ID AAH34142 PRELIMINARY; PRT; 240 AA.  
AC AAH34142;  
DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RA Strausberg R.;  
RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; BC034142; AAH34142.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 240 AA; 26234 MW; 188D4DD8BB781EC4 CRC64;

Query Match 63.8%; Score 441.5; DB 2; Length 240;  
Best Local Similarity 66.2%; Pred. No. 1.7e-34;  
Matches 88; Conservative 17; Mismatches 27; Indels 1; Gaps 1;

QY 1 MMSPAQFLFLLVLWIRETNGYVMTQTPLTSLVTIGQPASISCKSSQSLLDSGKTYLW 60  
| ||| | ||:|: ::| :|| |:|:|||| |:|||||:||||| |:| | :|

Db 1 MRLPAQLLGLLMLWVSGSSGDIVMAQSPLSLSVTPGEPASISCRSSQSLLHSNGYNYFDW 60

QY 61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLTKISRIEADLGLYYCWQGTHF- 119



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      ||:||||: ||| | |||||:|||||||:||||:|:| | |
Db      61 YLQKPGQSPQLLIYWGSNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP 120

Qy      120 PRTFGGGTKLEIK 132
      | ||| |||||
Db      121 PYTFGQGTKLEIK 133

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RESULT 15

AAR11017

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ID  AAR11017      PRELIMINARY;      PRT;      114 AA.
AC  AAR11017;
DT  02-MAR-2004 (TrEMBLrel. 27, Created)
DT  02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT  02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE  ANA immunoglobulin kappa light chain (Fragment).
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=B6.Sle1; TISSUE=Spleen;
RA  Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT  "Antinuclear autoantibodies from B6.Sle1 mice.";
RL  Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
DR  EMBL; AY436857; AAR11017.1; -.
FT  NON_TER      1      1
FT  NON_TER      114     114
SQ  SEQUENCE      114 AA; 12422 MW;  C94A4DDCF55E8A8C CRC64;

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Query Match      63.0%; Score 436; DB 2; Length 114;
Best Local Similarity 75.2%; Pred. No. 2.5e-34;
Matches 82; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

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```

Qy      24 MTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDSGV 83
      |||||:| |:| ||||:||||: |:| ||| | |:||||| ||| || |||
Db      1 MTQTPLSLPVS LGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVS NRFSGV 60

Qy      84 PDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGT HFPRTFGGGTKLEIK 132
      |||:|||||||:|||||:||||:|:| | |||||
Db      61 PDRFSGSGSGTDFTLKISRVEAEDLG VYYCFQGSHPWTFGGGTKLEIK 109

```

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Job time : 127.644 secs